STIC-Biotech/ChemLib

From: Sent:

Slobodyansky, Elizabeth Thursday, June 19, 2003 12:24 PM STIC-Biotech/ChemLib 09/889,609

To:

Subject:

Please search for case 09/889,609:

SEQ ID NOs: 1 and 8-10 against commercial and interference databases.

Thank you.

Elizabeth Slobodyansky, PhD

Primary Examiner

Art Unit 1652 CM1 10D11 703-306-3222

mail box 10D01

Mary Jane Ruhl Tech. Info. Specialist, STIC TC-1600 CM-1, Room 6A-06 Phone: 605-1155

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

DB

Length

Query

Score

Result No.

100.0

1023 1023 1021.4 1020

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June 24, 2003, 06:24:52:; Search time 2668 Seconds (without alignments) 11158.984 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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A75951 S.cerevisia AP004826 Staphyloc G32814 A009527 Hum AP003189 Clostridi AP00982 Sulfolobu AE001716 Thermotog AP003133 Staphyloc

AE010646 Fusobacte AC095280 Rattus no AP000061 Aeropyrum AL139076 Campyloba AY052059 Drosophil

CJ11168X3 AY052059

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100.2 98.4 97.8 96.6 96.6 94.4 92.8

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Streptomy Ralstonia Pseudomon

AF096281 Arabidops AF177212 Arabidops AY065037 Arabidops

AP003362 Staphyloc AP003581 Nostoc sp AP000991 Thermopla

AC122087 Rattus no AL022245 S.pombe c AL031603 S.pombe c Z28218 S.cerevisia

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142 137 131.4 128.4 126.2 126

BC031531 AC122087

181.6 181.6 180 176.2 157.6 157.6 157.2

AC044847 Mus muscu BC031531 Mus muscu

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AR026565 Homo sapi AK026565 Homo sapi AL450226 Homo sapi AC021705 Homo sapi

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AL834378 Homo sapi AF148321 Mus muscu BC011164 Mus muscu BC019090 Homo sapi

AK023169 Homo sapi AX259575 Sequence AX224420 Sequence

AY034081 Homo sapi AF169974 Homo sapi AX224418 Sequence

Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo 1 (bases 1 to 1023)
Xia,M., Liu,Y. and Connolly,T.M.
Molecular cloning and expression of human serine racemase from human NT2N cells REFERENCE AUTHORS TITLE is the number of results predicted by chance to have a

Pred. No.

PRI 01-JUN-2002

linear

Arusqubl 1023 bp mRNA lines Homo sapiens serine racemase mRNA, complete cds. Ar034081

AY034081.1 GI:21307620

VERSION KEYWORDS SOURCE ORGANISM

DEFINITION ACCESSION

RESULT 1 AY034081

LOCUS

ALIGNMENTS

780 840 840 900 900 960 960

999

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PRI 27-0CT-2000
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RMKLLIEPTAGVGVAAVLSQHFQTVSPEVKNICIVLSGGNVDLTSSITWVKQARRPAS
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Direct Submission
Submitted (18-JUL-1999) Departamento de Bioquimica Medica,
Instituto de Clencias Blomedicas, Universidade Federal do Rio de
Janeiro, Av. Brigadeiro Trompowski, s./n, Rio de Janeiro 21491-590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1166)
De Miranda,J., Santoro,A., Engelender,S. and Wolosker,H.
Human serine racemase: moleular cloning, genomic organization and
                                  AAGCTGAAGGGGAAACTGATGCCCAATCTTTATCCTCCAGAAACCATAGCAGATGGTGTC
       AAACCTAGTGTGAAGGTATATGCTGTGAACCCTCAAATGCAGATGACTGCTACCAGTCC
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Gene 256 (1-2), 183-188 (2000)
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RMKLLIEPTAGVGVAAVLSQHFQTVSPEVKNICIVLSGGNVDLTSSITWVKQAERPAS
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Xia.M., Liu.Y. and Connolly.T.M.
Direct Submission
Submitted (08-MX-2001) Pharmacology, Merck & Co.,
West Point, PA 19486, USA
Location/Qualifiers
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i i i	Match 100.0%; Score 1023; DB 9; Length 1166; Local Similarity 100.0%; Pred. No. 6.5e-266; Local Similarity 0; Mismatches 0; Indels 0; Gaps 0;	Qy Dp	1021 TAA 1023
Qy Db	1 ATGTGTCAGTATTGCATCTCCTTTGCTGATGTTGAAAAAGCTCATATCAACATTCGA 60 	RESULT 3 AX22418 LOCUS	AX224418
oy Db	61 GATECTATÈCACCTCACACCAGTGCTAACAAGCTCCATTITGAATCAACTAACAGGGGC 120 	DEFINITION ACCESSION VERSION KEYWORDS	Sequence 1 from Patent AX224418 AX224418.1 GI:1555466
Qy Dp	121 AATCTTTCTTCAATGTGAACTCTTCCAGAAACAGGATCTTTAAGATTCGTGGTGCT 180 	SOURCE ORGANISM	
da	181 CTCAATGCCGTCAGAAGCTTGGTTCCTGATGCTTTAGAAAGGAAGCCGAAAGCTGTTGTT 240 	KEFEKENCE AUTHORS TITLE	<pre>1 (Dases 1 to 1//0) Meyers,R.A. and Rudolph-Owen,L.A. A human pyridoxal-phosphate dependent enzyme family member and uses therefor</pre>
Oy Dp	241 ACTCACAGCAGTGGAAACCATGGCCAGGCTCTCACCTATGCTGCCAAATTGGAAGGAA	JOURNAL FEATURES SOUR	. 0
Qy Dp	301 CCTGCTTATATTGTGGTGCCCGAGAGGCTGCAGACTGTAAAAACTTGCAATACAAGCC 360 	CDS	/organism="Homo sapiens" /db_xref="taxon:9606" 691091 /note="unnamed protein product"
Qy Db	361 TACGGAGCGTCAATTGTATACTGTGAACCTAGTGATGCCAGAGAAAATGTTGCAAAA 420 		/codon_start=1 /protein_io="Cac69570.1" /db_xref="GI:15554661" /translation="MCAQYCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFF
cy Op	421 AGAGTTACAGAAGAGAGAGATCATGGTACATCCCAACAGGAGCCTGCAGTGATA 480 		KCELFOKTGSFKIRGALNAVRSLVPDALERKPRAVTHSGRHGQALTYAAKLEGIPA YIVVPQTAPDCKKLAIQAYGASIVYCEPSDESRENVAKRYTETEGIMVHPNQEPAVI AQQGTIALEVLNOVPLVPDALVVPVGGGGMLAGIATIVKALKPSVKVYAAEPSNADDCY QSKLKGKLMPNLYPPETIADGVKSSIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWE
Oy Db	481 GCTGGACAAGGGACAATTGCCCTGGAAGTGCTGAACCAGGTTCCTTTGGTGGATGCACTG 540 	BASE COUNT ORIGIN	499 a
oy Dp	541 GTGGTACCTGTAGGTGGAGGAATGCTTGCTGGAATAGCAATTACAGTTAAGGCTCTG 600 	Query Match Best Local Matches 102	/ Match 100.0%; Score 1023; DB 6; Length 1770; Local Similarity · 100.0%; Pred. No. 6.4e-266; Length 1770; Local Similarity · 100.0%; Pred. No. 6.4e-266; Length 1770; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
oy B	601 AAACCTAGTGTGAAGGTATATGCTGCAACCCTCAAATGCAGATGACTGCTACCAGTCC 660 	Qy Db	I ATGTGTGCTCAGTATTGCATCTCTTTGCTGAAGTTGAAAAGCTCATATCAACATTCGA 60
oy Db	661 AAGCTGAAGGGAAACTGATGCCCCAATCTTTATCCTCCAGAAACCATAGCAGATGGTGTC 720 	Qy	61 GATTCTATCCACCTCACACCAGTGCTAACAAGCTCCATTTTGAATCAACTAACAGGGGG 120
oy Og	721 AAATCCAGCATTGGCTTGAACACCTGGCCTATTATCAGGGACCTTGTGGATGATATCTTC 780 	, QQ	121 AATCTTTCTTCAAATGTGAACTCTTCCAGAAAACAGGATCTTTTAAGATTCGTGGTGCT 180
ò da	781 ACTGTCACAGAGGATGAAATTAAGTGTGCAACCCAGCTGGTGGGGAGAGGATGAACTA 840 	Oy Db	181 CTCAATGCCGTCAGAAGCTTGGTTCCTGATGCTTTAGAAAGGAAGCCGAAAGCTGTTGTT 240
oy Oy	841 CTCATTGAACCTACAGCTGTTGGAGTGGCTGCTGTGCTG	Qy	241 ACTCACAGCAGTGGAAACCATGGCCAGGCTCTCACCTATGCTGCCAAATTGGAAGGAA
Qy	901 GTTTCCCCAGAAGTAAAGAACATTGTATTGTGCTCAGTGGAAATGTAGACTTAACC 960 	Qy	301 CCTGCTTATATTGTGGTGCCCCAGACAGCTCCAGACTGTAAAAAACTTGCAATACAAGC 360
Qy	961 TCCTCCATAACTIGGGTGAAGCAGGCTGAAAGGCCAGCTTCTTATCAGTCTGTTTCTGTT 1020	Qy	TACGGAGCGTCAATTGTATACTGTGAACCTAGTGATGAGTCCAGAGAAAATGTTGCAAAA

121 AAATCCAGCATTGGCTTGAACACCTGGCCTATTATCAGGGACCTTGTGGATGATATCTTC 780 781 ACTGTCACAGAGGATGAAATTAAGTGCAACCCAGCTGGTGGGGAGGGA		Berlin-Charlottenburg, GERWANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/. Location/Qualifiers 1. 2264 / Organism="Homo sapiens" / Ab_xref="taxon:9606" / Amp="22.9 or R from top of Chrl7 linkage group" / Clone="lbxEzp762A215" / Clone="brEzp762A215" / Clone="brEzp762A215" / Acv_stage="adult" / Acv_stage="adult" / Acv_stage="adult" / BH10B: sites Not1 + Sall" / Acv_stage="adult" / Acv_stage="adult" / Acv_stage="adult" / Bh10B: sites Not1 + Sall" / Acv_stage="brEzp762A215" / Acv_stage="adult" / Acv_stage="adult" / Acodon_start=1 / Aponte="hypothetical protein" / Ab_xref="G1:21740049" / Ab_xref="G1:21740049
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	RESULT 7 HSM805450 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	FEATURES SOUTCE GENE CDS . POlyA POLYA
AX224420.1 GI:15554662 human. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1020) Meyers, R.A. and Rudolph-Owen, L.A. A human pyridoxal-phosphate dependent enzyme family member and uses therefor Wo 0160987-A 3 23-AuG-2001; Millennium Pharmaceuticals, Inc. (US) Location/Qualifiers 1. 1020 / Organism="Homo sapiens" /db_xref="taxon:9606" F 288 a 220 c 243 g 269 t	99.7%; Score 1020; DB 6; Length 1020; 5: Conservative 0; Mismatches 0; Indels 0; Gaps ATGTGTGCTATTGCATCTCTTGCTGATGTTGAAAAAGCTCATATCAACATTGA ATGTGTGCTCAGTATTGCATCTCCTTTGCTGATGTTGAAAAAGCTCATATCAACATTGA ATGTGTGCTCAGTATTGCATCTCCTTTGCTGATGTTGAAAAAGCTCATATCAACATTGA GATTCTATCCACCACCACCACTGCTAACAACGTCCATTTTGAATCAACAACAGCGCGC	241 ACTCACAGCAGTGGAAACCATGGCCCCAGCTTCACCTTATGCTGCCAAATTGGAAGGAA
VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	Ψ̈́Ŏς	

VERSION AF148321.1 GI:6448864 KEYWORDS	Σ	1 (bases 1 to 1197) Wolosker, H., Blackshaw, S. and Snyder, S.H. Serine racemase: a glial enzyme synthesizing D-seri glutamate-N-methyl-D-aspartate neurotransmission	JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (23), 13409-13414 (1999) MEDLINE 20027561 PUBMED 10557334 REFERENCE 2 (bases 1 to 1197)	Wolosker,H Direct Submission Submitted (03 MAY-1999) Neu North Wolfe St., WBSB 806,	cul	/db_xref="taxon:10090" CDS 66. 1.085 /EC_number="5.1.1.17" /function="catalyzes L-serine to D-serine racemization"	/codon_start=1 /product="serine racemase" /protein_id="AAF08701.1" /db_xref="GI:6448865"	/translation="WCAQYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFF KCELFQKTGSFKIRGALMAIRIGALTYARSGNHGQALTYARAKLECIPA YTVVPQTARPKCKLANIQARQAYOASIVYCDPSDESREKYTQRINQETEGILYHPNQEPAVI AGQGTIALEVLNQVPLVDALVVPVGGGGWVAGIAITIKALKPSVKVYAAEPSNADDCY	QSKLKGELTPNLHPPETIAGGVKSSIGLNTWPIIRDLVDDVFTVTEDEEKYATGLVWG RMKLLIEPTAGVALAAVLSQHFQTVSPEVKNVCIVLSGGNVDLTSLNWVGQAERPAPY QTVSV" BASE COUNT 345 a 283 c 283 g 286 t	/ Match 79.8%; Score 816.6; DB 10; Length 1197; Local Similarity 88.1%; Pred. No. 5e-210;	Matches 901; Conservative 0; Mismatches 119; Indels 3; Gaps 1 ATGTGTGCTCAGTATTGCATCTCCTTTGCTGAAAAAGCTCATATCAACATTCGA	6 ATGTGTGCTCAGTACTGCATCTCCTTTGCTGATGTTGAAAAAGCTCATATCAACATTCAA 61 GATTCTATCCACCACCACAGCGGCTAACAAGCTCCATTTTGAATCAACTAACAGGGGG 11 111111111111111111111111111111	126 GACTCTATCCACCTCACCCCAGTGCTAACAAGCTCCATTTTGAATCAAATAGCAGGGGGCC 121 AATCTTTCTTCAAATGTGAACTCTTCCAGAAAACAGGATCTTTTAAGATTCGTGGTGCT	186 AATCTTTCTTCAAATGTGAGCTCTTTCAGAAAACTGGGTCTTTTAAGATTCGAGGTGCC 24 181 CTCAATGCCGTCAGAAGCTTCGTTCCTGATGCTTTAGAAAGGAAGCCGAAAGCTGTTGTT 24 11 11111 11111 1111 11111 111111 1 11111	246 CTTAATGCCATCAGAGGCTTAATTCCTGACACGCCAGAAGAAGCACCAAAGCCCGTAGTT 30 241 ACTCACAGCAGGGAACCATGGCCAGGCTCTCACCTATGCTGCCAAATTGGAAGGAA	206 ACTCACAGCAGAAACCATGGCCAAGCTCTCACCTATGCTGCTAAACTGGAAGGAA	361 TACGGAGCGTCAATTGTATACTGTGAACCTAGTGATGAGTCCAGAGAAAATGTTGCAAAA	Qy 421 AGAGTTACAGAAGAAACAGAAGCATCATGGTACATCCCAACCAGGAGCCTGCAGTGATA 480
BASE COUNT 692 a 478 c 465 g 629 t ORIGIN	Query Match 84.8%; Score 867; DB 9; Length 2264; Best Local Similarity 100.0%; Pred. No. 1.1e-223; Matches 867; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 157 GGATCTTTTAAGATTCGTGGTGCTCTCAATGCCGTCAGAAGCTTGGTTCCTGATGCTTTA 216	QY 217 GAAAGGAGGCGAAAGCTGTTGTTACTCACAGGGGGAAACCATGGCCAGGCTCTCACC 276 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 277 TATGCTGCCAAATTGGAAGAATTCCTGCTTATATTGTGGTGCCCCAGACAGCTCCAGAC 336	QY 337 TGTAAAAACTTGCAATACCAAGCCTACGGAGCGTCAATTGTATACTGTGAACCTAGTGAT 396	QY 397 GAGTCCAGAGAAAATGTTGCAAAAAGGTTACAGAAGAAACAGAAGGCATCATGGTACAT 456 	OY 457 CCCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGGACAATTGCCCTGGAAGTGCTGAAC 516	Qy · 517 CAGGTTCCTTTGGTGGATGCACTGGTGCTGCAGGAGGAGGAATGCTTGCT	OY 577 ATAGCAATTACAGTTAAGGCTCTGAAACCTAGTGAAGGTATATGCTGCTGAACCCTCA 636	OY 637 AATGCAGATGACTGCTACCAGTCCAAGGGGAAACTGATGCCCAATCTTTATCCT 696	Oy 697 CCAGAAACCATAGCAGGTGTCAAATCCAGCATTGGCTTGAACACCTGGCCTATTATC 756 	Qy 757 AGGGACCTIGIGGATGATATCTTCACIGICACAGAGGAIGAAATTAAGIGIGCAACCCAG 816 	Qy 817 CTGGTGTGGGGAGGATGAAACTACTATTGAACCTACAGCTGGTGTGGAGTGGCTGCT 876	QY 877 GTGCTGTCAACATTTTCAAACTGTTTCCCCAGAAGTAAAGAACATTGTATTGTGCTC 936 	OY 937 AGTGGTGGAAATGTAGACTTAACCTCCTCATAACTTGGGTGAAGCAGCTGAAAGGCCA 996 11111111111111111111111111111111111	Oy 997 GCTTCTTATCAGTCTGTTTAA 1023 	AF148321 1197 bp mRNA lines	DEFINITION MUS MUSCULUS SETINE FACEMASE MRNA, COMPLETE CAS. ACCESSION AF148321

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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Scries: IRAR Plate: 24 ROW: m Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7305520. Location/Qualifiers
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RMKLLIEPTAGVALAAVLSQHFQTVSPEVKNVCIVLSGGNVDLTSLNWVGQAERPAPY
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                      Hulyk, S.W., Hale, S.M.,
Martin, R.G., Muzny, D.M.
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Pred. No. 4.9e-210;
0; Mismatches 119;
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                      × ×
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288. 1307
                     Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
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                                                                                                                                                                                                      /organism="Mus musculus"
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       Contact: amg@bcm.tmc.edu
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Sciurognathi; Muridae; Murinae; Mus
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GTGGTACCTGTAGGTGGAGGAGGAATGCTTGCTGGAATAGCAATTACAGTTAAGGCTCTG
                                                  GCTGGACAAGGGACAATTGCCCTGGAAGTGCTGAACCAGGTTCCTTTGGTGGATGCACTG
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Mus musculus, Similar to serine ra
IMAGE:4195695, mRNA, complete cds.
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Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
1 (bases 1 to 1411)
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BC011164.1 GI:15029880
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Web site: http://www.]
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing Center
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AUTHORS
TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"Unknown (protein for MGC:29514)"
/protein_id="AAH19090.1"
/d_xref="G1:1751218"
/translation-"MAKVADTILFLLDPLEGMDSTGDYCLSCLFAOGLPTYTLAVQGI SGLPLKKQIDTRKKLSKAVERFPHDKLLLLDTQQEAGMLLRQLANOKQQHLAFRDRR
                                                                                       information can be found
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 14-MAR-2000
                                                                                     Clone distribution: MGC clone distribution information can be foun through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 39 Row: j Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8922495.
Tiongson, E. E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        863 TTGGAGTGGCTGCTGTGTCTCAACATTTTCAAACTGTTTCCCCAGAAGTAAAGAACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    923 TTTGTATTGTGCTCAGTGGTGGAAATGTAGACTTAACCTCCCATAACTTGGGTGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagase,T., Kikuno,R., Ishikawa,K.I., Hirosawa,M. and Ohara,O. Prediction of the coding sequences of unidentified human genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         brain cDNA to mRNA, clone_lib:pBluescriptII SK
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                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Brain, neuroblastoma"
/clone_lib="NIH_MGC_19"
/lab_host="DH10B-R"
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Pred. No. 8.4e-49;
                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9606"
/clone="MGC:29514 IMAGE:4896567"
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                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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AB037822
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pOTB7"
319. .2289
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clone:hk09639.
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Homo sapiens, clone MGC:29514 IMAGE:4896567, mRNA, complete cds.
BC019090
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Shevchenkv,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
     GCTGGACAAGGAACAATTGCCCTGGAAGTGCTGAACCAGGTTCCCTTGGTAGATGCACTG 827
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Submitted (07-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                AAACCTAGTGTGAAGGTATATGCTGCTGAACCCTCAAATGCAGATGACTGCTACCAGTCC
                                                                                                                                                                                                       GTTTCCCCAGAAGTAAAGAACATTTGTATTGTGCTCAGTGGTGGAAATGTAGACTTAAACC
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                                                       GTGGTACCTGTAGGTGGAGGAGGAATGCTTGCTGGAATAGCAATTACAGTTAAGGCTCTG
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Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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KEYWORDS
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Homo sapiens
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                                                                                                ORGANISM.
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HSBC17A99/c
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RHRASQLARQKERVLAEKRQLGGRDGPHQVLVVPLHSRISIPEAMOLLQDRDTGV
RHRASQLARQKERVLAEKRQLGGRDGPHQVLVVPLHSRISIPEAMOLLQDRDTGTV
HLNELGNTQNFMLLCPRLKHRWFTRARPGDLHVVLDMAKVAPOTILFLLDDFLEGWBST
GDYCLSCLEPAGLPTYTLAYQGISGLELKKQIDTRKKLSRAYERFPHDKLLLLDTGQ
EAGMLLHVGYGDFQWKQIDAFQDFPLNKGITRVQKDDDMAMETCATADAYDDMEDELKV
NRLLHIVGYGDFQWKQIDAPGDFPPLNKGITRVQKDFDNAMETCATADAYDDMEDELKV
LMRADPGROESLQAEVIPDPMGSEQTWPTEEELSEAKDFLKSSKVVKKYPRGTSSYQ
AFWILDGSGSGGGEDET RYDDMEHEDFSQDGSSEEEEFYETWTIGESVHDDLY
DKKVDEGABAKMLEKYKGERLEMFDDEVJFRDVAARIRFQKTSSWDDLY
GTPLLAFSLLPHPGSKMSVLMVYRRDFGTRPYRAZELFFFRG
AVI. The complete sequences of 150 new cDNA clones from brain which
DNA Res. 7 (1), 65-73 (2000)
                                                                                                                                      Direct Submission
Submitted (31-JAN-2000) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:http://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="HGALTSCWKRPSREGAGSPAPWRARPLGGDRKRLSWPGSSADSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AADKHKLQRPLTADMALVATVYAPITFPPASVILLFKOKSNGMHSLIATGHLMSVDPDR
MVIKRVVLSGHPFKIFTKMAVVRYMFFNREDVLWFKPVELRTKWGWRGHIKEPLGTHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      923 TITGTATTGTGCTCAGTGGTGGAAATGTAGACTTAACCTCCTCCATAACTTGGGTGAAGC 982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HMKCSFDGKLKSQDTVLMNLYKRVFPKWTYDPYVPEPVPWLKSE1SSTVPQGGME"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       803 AGTGTGCAACCCAGCTGGTGTGGGAGGATGAACTACTACATTGAACCTACAGCTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.6%; Score 221; DB 9; Length 4107; 100.0%; Pred. No. 8.3e-49; ive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4140 bp mRNA linear
Homo sapiens cDNA: FLJ22912 fis, clone KAT06132.
AK026565.
AK026565.1 GI:10439447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Start codon.is not identified."
                                                                                                                                                                                                                                                                                                                                           SK plus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="KIAA1401 protein"
                                                                                                                                                                                                                                                                                                                          /tissue_type="brain"
/clone_lib="pBluescriptII
                                                                                                                                                                                                                                                                        /organism~"Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="BAA92639.1"
/db_xref="GI:7243183"
                                                                                                     2 (bases 1 to 4107)
Ohara, O., Nagase, T. and Kikuno, R.
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                         /clone="hk09639"
                                                                                                                                                                                                                                                                                                                                                                          /gene="KIAA1401"
                                                                                                                                                                                                                                                                                                                                                                                          <934. .3495
/gene="KIAA1401"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
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AK026565/c
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Submitted (29-MGC2000) Sumio Sugano, Institute of Medical Science, Submitted (22-MGC2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center: Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnad@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2929
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Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Nakamura,Y., Isogai,T. and Sugano,S.
                                                                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T., Shibahara, T., Tanaka, T. and Nakamura, Y. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L23454 bp DNA linear PRI 17-NOV-:
Homo sapiens chromosome 17 sequence from PAC RPCI-5 1037N22 map
AL450226 AL137039
AL450226.1 GI:11228434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTGTATTGTGCTCAGTGGTAAATGTAGACTTAACCTCCTCCATAACTTGGGTGAAGC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cell_type="signet_ring cell carcinoma"/clone_lib="KAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             983 AGGCTGAAAGGCCAGCTTCTTATCAGTCTGTTTCTGTTTAA 1023
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hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="cloning vector pME18SFL3"
901 c 1050 g 994 t
oligo capping; fis (full insert sequence)
                        Homo sapiens signet-ring cell carcinoma mRNA, clone_lib:KAT clone:KAT06132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
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KEYWORDS
SOURCE
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Libraticed (19-JAM-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (Dases I to 221909)

Barran, Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barran, A., Chang, J., Chazaro, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Lindblad-Toh, K., Lindblad-Toh, K., Liudblad, S., Karatas, A., Kalas, C., Landers, T., Levine, R., Lindblad-Toh, K., Liuds, MacLean, C., Macdonald, P., Major, J., Matthews, C., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., Nurphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C., Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, R., Schauer, B., Standen, S., Sewery, P., Smith, C., Spencer, B., Stange-Thoman, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, B., Wayman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Zembek, L., Zimmer, A. and Zody, M.
                               Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., MeBwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pisan, L.C., Pollara, V., Raymond, C., Riley, R., Cothman, D., Stojanovic, N., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Direct Submission
         Jones, C., Kann, L., Karatas, A., Klein, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (23-3406-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 23, 2002 this sequence version replaced 91:22296935.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69249 69348: gap of 100 bp 69349 69349 2592: contig of 23244 bp in length 92593 92692: gap of 100 bp 92693 221909: contig of 129217 bp in length. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49593 49692: gap of 100 bp
49693 65686: contig of 15994 bp in length
65687 65786: gap of 100 bp
65787 69248: contig of 3462 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www-seq.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: L5879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: 380_H_7
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      Howland, J.C., Johnson, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="17"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG.23-AUG-2002
*** SEQUENCING
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boguslavkly, L., Boukhqalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Perreira, P., Etzrlugh, W., Fornest, C., Gage, D., Galagan, G., Grant, G., Hagos, B., Heaford, A., Horton, L., Galagan, J.,
                                                                                                                                                                                                 Direct Submission
Submitted (20-JAN-2000) MOLGENR, Abt.Lehrach, Max Planck Institut
Fuer Molekulare Genetik, Innestrasse 73, Berlin, 14195 Germany
Contiq 01
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                         Ramser,J., Langer,I., Klein,M., Arndt,S., Lehrack,S., Junker,E.,
Schuelzchen,S., Noitz,M., Thompson,C., Hoff,C., Poustka,A.,
Reinhardt,R. and Lehrach,H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       803 AGTGTGCAACCCAGCTGGTGTGGAAGATGAAACTACTCATTGAACCTACAGCTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGGAGTGGCTGCTGTCTCTCAACATTTTCAAACTGTTTCCCCAGAAGTAAAGAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone_lib="RPCII,3-5, Roswell Park Cancer Institute, creator Pieter de Jong, P.Ioannou" /note="region between markers D178695 - D178654"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.6%; Score 221; DB 9; Length 123454; 100.0%; Pred. No. 7e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens chromosome 17 clone RP11-380H7 map 17, IN PROGRESS ***, 5 unordered pieces.
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HTG; HTGS_PHASE1; HTGS_FULLTOP; HTGS_ACTIVEFIN.
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Birren,B., Nusbaum,C. and Lander,E.
Unpublished
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31233 a 26833 c 28651 g 36737 t
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Matches 221; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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1. .123454
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /map="17q13.3"
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2 (bases 1 to 123454)
MOLGENR.
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Birect Submission

AL Submitted (14-MAR-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (14-MAR-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (14-MAR-2002) Wellcome requests: clonerequest@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Mar 21, 2002 this sequence version replaced gi:17902958.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >- 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSROT; Tr:, TREMBL; WP:, WORWPEP; Information on the WORWPEP
                                                                                                                                                                                                                  AL604066 184151 bp DNA linear ROD 14-MAR-2002 Mouse DNA sequence from clone RP23-174M12 on chromosome 11, complete sequence.
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                                                                                                                                                                                       803 AGTGTGCAACCCAGCTGGTGTGGAAGAGGATGAAACTACTCATTGAACCTACAGCTGGTG 862
                                                                                                                                                                                                                                                                                               863 ITGGAGTGGCTGCTGTGTCTCAACATTTTCAAACTGTTTCCCCCAGAAGTAAAGAACA 922
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 184151)
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This sequence is the entire insert of clone RP23-174M12 The true
right end of clone RP23-194P5 is at 82810 in this sequence.
                                                                                                                                           Gaps
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                                                                               Length 221909;
     415 others
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                                                                               Score 221; DB 2; I
Pred. No. 6.8e-49;
                                                            21.6%; Sco. 100.0%; Pred. No. c. 0; Mismatches
53146 a 52419 c 54384 g 61545 t
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1. .184151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL604066
AL604066.9 GI:19571943
                                                                                                                                   Matches 221; Conservative
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                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
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                                                                               Query Match
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/organism="Mus musculus" /db_xref="taxon:10090" /chromosome="11" /clone="RP23-174M12"

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772
                                                                                                                                                                               653 ACCAGTCCAAGCTGAAGGGGAAACTGATGCCCAATCTTTATCCTCCAGAAACCATAGCAG
                                                                                                                                                                                                                                           713 ATGGTGTCAAATCCAGCATTGGCTTGAACACCTGGCCTATTATCAGGGACCTTGTGGATG
                                                                                                                     593 AGGCTCTGAAACCTAGTGTGAAGGTATATGCTGCTGAACCCTCAAATGCAGATGACTGCT
                                                                                         Gaps
                                                        Length 184151;
                                             Score 181.6; DB 10; Lower Pred. No. 3.2e-38;
                                                                                                                                                                                                                                                                                                                     773 ATAICTICACTGTCACAGAGGATGAAATTAAG 804
                                                                                       0; Mismatches
/clone_lib="RPCI-23"
46879 a 41019 c 43482 g 52771
                                                          17.8%;
                                                                      91.08;
                                                                                      Matches 193; Conservative
                                                                         Similarity
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BI739030 603359880 BQ885621 AGENCOURT BI738966 603359780 AV022510 AV022510 AV374491 AV374491 BM719814 UI-E-EJO-AI322578 mi51e12.y BG965678 602830522 BG404240 602420304

AA446793 zw89f62.r B1332919 602984289 BB692466 BB692486 BF135412 601784509 BB641631 BB641631 AV709023 AV709023 AV649313 AV649313 BB625125 BB625125 AA6434539 mis51et2.r BB621410 BB621410 BF532321 602073350

Title: Perfect score:

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Scoring table:

Searched:

Minimum DB Maximum DB

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konoo, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs io prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (strain:C57BL/6J) adult male pituitary gland cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library clone:5330405D10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AK017235 1398 bp mRNA linear Mus musculus adult male pituitary gland cDNA, RIKEN enriched library, clone:5330405D10:serine racemase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9279253
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                                                                                                                             AI322578
BG965678
BG404240
AA446793
                                 BQ885621
BI738966
AV022510
                                                                                                                                                                                                                          BB692486
BF135412
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AV709023
AV649313
BB625125
AA034539
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BF532321
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BB644584
BQ2133565
BQ213565
BQ303566
AW319255
BB618702
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HTC 19-JAN-2002 full-length full insert

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CDNA was cleaved
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
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                            with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGCTTACATTGTGGTTCCCCAAACAGCTCCCAACTGCAAGAAACTGGCAATCCAAGCC
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0; Mismatches 5;
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/db_xref="taxon:10090"
/clone="5330405D10"
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336 c 340 g 326 t
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/strain="C57BL/6J"
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Best Local Similarity 99.4%;
Matches 1010; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S. Adachl, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Saraka, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hangaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itch, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kouda, M., Koyai, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, H., Saito, H., Sasaki, C., Sano, H., Sasaki, D., Schrinl, L., Shibata, K., Shibata, Y., Shinagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamannka, I., Yasunishi, A., Yoshino, M., Muramatsu, M. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute: 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-reségsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. Sequencing pipeline with 384 multicapillary sequencer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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                      AUTHORS
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BI763753 785 bp mRNA linear EST 25-SEP-2001 603047780F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:5188099 5',
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1 (bases 1 to 785)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) (Dnpublished (1999)

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Email: cgapbs-rémail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Lncyte Genomics, Inc.
                                  1 ATGTGTGCTCAGTACTGCATCTCCTTTGCTGATGTTGAAAAAGCTCATATCAACATTCAA
                                                                                                                                                                                                                                    CTATGGAGCATCGATAGTATACTGTGACCCAAGTGACGAGTCCAGAGAAAAGGTCACTCA
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                                                                  40 ATGTGTGCTCAGTACTGCATCTCCTTTTGCTGATGAAAAAGCTCATATCAACATTCAA
                                                                                                   GACTCTATCCACCTCACCCCAGTGCTAACAAGCTCCATTTTGAATCAAATAGCAGGGCGC
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                               BF163794 1769 bp mRNA linear EST 30-OCT-2000 00.769701F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3988873 5',
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11 (bases 1 to 769)
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13 (bases 1 to 769)
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                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM9198 row: a column: 02
High quality sequence stop: 699.
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Stem cell origin."
/lab_host="DH10B"
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                                                                                                                                                                  ACTGTCACCGAAGATGAAATCAAGTATGCAACCCAGCTGGTGTGGGGGGAATGAAACTG
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Pred. No. 3e-183;
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/strain="C2ECH II"
/db_xref="taxon:10090"
/clone="INAGE:3988973"
/clone=lib="NCI_CGAP_Lu29"
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AUTHORS
TITLE
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187 c 214 g 207 t 4 others
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1 (bases 1 to 848)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Makamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                      CTTGTGGATGATGTCTTCACTGTCACCGAAGATGAAATCAAGTATGCAACCCAGCTGGTG
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Unpublished (2000)
Contact: Takao Isogai
Genmics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Pax: 81-438-52-3975
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3e-170;
ches 93; I
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Pred. No. 3e-17
0; Mismatches
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/db_xref="taxon:9606"
/clone="NT2RP3002501"
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11 Similarity 87.6%;
687; Conservative
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                                                                                                                                                                                              /note="Organ: pooled colon, kidney, stomach; Vector:
pCWV-SPORT6; Site_1: NotI; Site_2: ECCRV (destroyed); RNA
source anonymous pool of 3 colons, age 26 yo male, 49 yo
female, 71 yo male colon: 46 yo male kidney, and pool of 2
stomachs, 62 yo male and 70 yo female. Library is
oligo-dT primed and directionally cloned (ECCRV site is
destroyed upon cloning). Average insert size 1.4 kb,
insert size range 1.3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
023. Note: this is a NIH_MGC Library."
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Clone distribution: MGC clone distribution information can
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             found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11469 row: p column: 20
High quality sequence stop: 783.
Location/Qualifiers
1. 785
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Pred. No. 1.5e-171;
0; Mismatches 92;
                                                                                                                                               /clone="IMAGE:5188099"
/clone_lib="NIH_MGC_116"
/lab_host="DH10B"
                                                                                                     Query Match 59.3%;
Best Local Similarity 87.9%;
Matches 692; Conservative
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168 C
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RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

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Y. and Hayashizaki,Y. Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinaqawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa Hayashizaki,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
A., Konno,H., Okazaki,Y., Mramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
penes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contributed to prepare mouse tissues. 1st strand cDNA was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="1190028F16"
/clone_lib="RIKEN full-length enriched, 18 days embryo"
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Please visit our web site (http://genome.gsc.riken.go.jp)
further details.
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Pred. No. 3.7e-169;
0; Mismatches 3;
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takawai, F., Takeda, Y., Tanaka, T., Toya, T., RIKEN, Mouse ESTS, (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB609829 RIKEN full-length enriched, 18 days embryo Mus musculus CDNA clone 1190028F16 5', mRNA sequence.
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17-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Pax: 81-45-503-9216
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JOURNAL
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KEYWORDS
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Dp 3		qq	6 ATGTGTGCTCAGTAC
0y 3	m	Qy	61 GACTCTATCCACCTC
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Qy 3			121 AATCTTTTCTTCAA?
Db 4	428 TATGGAGCATCGATAGTATACTGTGACCCAAGTGACGAGTCCAGAGAAAAGGTCACTCAA 487		126 AATCTTTTCCTCA
Qy 4	421 AGAATTATGCAAGAAACAGAAGGCATCTTGGTCCATCCCAACCAGGAGCCTGCAGTGATA 480 	Oy Dp	181 CTTAATGCCATCAGA 181 11 11 11 11 11 11
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Qy 5			301 CCTGCTTACATTGTC
9 qa	608 GTGGTACCAGTAGGAGGAGGAGGAGGATGGTTGCTGTAGTTACANTTAAGGCCCTG 667	e oo	306 CCTGCTTACATTGTG 361 TATGGAGCATCGATA
RESULT 6			
×	BI988879 600 bp mRNA linear EST 20-DEC-2001 4022-49 Mouse E14.5 retina lambda ZAP II Library Mus musculus CDNA,		421 AGAATTATGCAAGAA
ACCESSION VERSION	movs sequence. B1988879 B1988879 1 GT-17059868		
KEYWORDS SOURCE	e mouse.	do do	481 GCTGGACAAGGAACA
ORGANISM	Mus musculus Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Monumuaids, Educatid; Kodentid; Sciurognath; Muridae; Murinae; Mus. 1 (bases 1 to 60)	7S QQ	546 GTGGTNCCANTAGGA
TITLE	Multe,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H. Gene expression in the development retirs by rem commondia	r existed	
JOURNAL	and microarray amalysis Nucleic Acids Res. 29 (24), 4983-4093 (2001)	BE655084	70000
MEDLINE COMMENT	21671825 Contact: Klein WH	NOITI	DI-M-ALI-ahr-f-
	Department of Michemistry and Molecular Biology University of Texas M.D. Anderson Cancer Center		UI-M-ALL-ahr-f-12 BE655084 BE655084.1 GI:99
-	Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA Tel: 713 792 3646	KEYWORDS	EST. house mouse.
FEATURES	Fax: 713 790 0329. Location/Qualifiers	_	Mus musculus Eukaryota; Meta:
ao mos	/organism="Mus musculus"		Mammalia; Euthe 1 (bases 1 to
	/cone_lib="Mouse El4.5 retina lambda ZAP II Library"	AUTHORS	Bonaldo,M.F., Le Normalization an
	/Lissue_Lype="neural reting" /dev_stage="embryonic day 14.5 post-fertilization" /note="Vertor: pawp10 (Gibcol Clone midization");	JOURNAL	discovery Genome Res. 6 (9
	Primer: Oligo dr. RNA Isolation: cytoplasmic (Chantaris); Cloning Technique: CUA Cloning (CloneAmb.		9/0444// Contact: Chin, N National Institu
·÷	Life Technologies); Average insert size: 1.8 Kb; Insertion site: TAKGTCOACTGAATTGAAGTG Other		6001 Executive B1 20892-9643, USA
	<pre>intotmatton regarding entite library may be found at http://pga.swmed.edu/Data/Libraries/microarray_cdna_librar ies.htm "</pre>		Tel: 301 443 170 Fax: 301 443 989
BASE COUNT ORIGIN	177 a 145 c 134 g 136 t · 8 others	•	cDNA Library Prep Researchers may o
Query Mat Best Loca	oore 583.8; DB 13; Length 60 red. No. 1.5e-165;		should be noted tadditional specia
Matches	0	-	collaborative arr

1 ATGTGTGCTCAGTACTGCATCTCCTTTGCTGAAAAAGCTCATATCAACATTCAA 60

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565 bp mRNA linear EST 06-SEP-2000 .2-0-UI.r2 NIH_BMAP_MCO_N Mus musculus cDNA clone .2-0-UI 5', mRNA sequence.
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obtain BMAP CDNA clones from RESEARCH GENETICS. It
that Bento Soares is generating a small number of
ialized non-redundant arrays of BMAP CDNAS whose
11 be considered under appropriate and limited
                                    TCACCCCAGTGCTAACAAGCTCCATTTTGAATCAAATAGCAGGGGGC 120
                                                                                                            AATGTGAGCTCTTCCAGAAAACTGGGTCTTTTAAGATTCGAGGTGCC 180
                                                                                                                                                                                                                                                                                                                                TGGTTCCCCAAACAGCTCCCAACTGCAAGAAACTGGCAATCCAAGCC 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAATTGCCCTGGAAGTGCTGAACCAGGTTCCCTTGGTAGATGCACTG 540
ACTGCATCTCCTTTGCTGATGTTGAAAAAGCTCATATCAACATTCAA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    coa; Chordata; Craniata; Vertebrata; Euteleostomi;
fia; Rodentia; Sciurognathi; Muridae; Murinae; Mus
665)
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                                                         SAGGCTTAATTCCTGACACGCCAGAAGAGAAGCCCAAAAGCCGTAGTT
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31vd. Room 7N-7190, MSC 9643, Bethesda,
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Seq primer: M13 Reverse.
Location/Qualifiers
1. .565
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Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      273 ATGTGTGCTCAGTACTGCATCTCCTTTGCTGATGTTGAAAAAGCTCATATCAACTTCAA 332
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                    Euteleostomi;
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             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleoston Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; I (bases 1'to 81)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) (npublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
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                                                                                                                                                                                                          DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information of found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM1933 row: p column: 19
High quality sequence stop: 817.
Location/Qualifiers
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Pred. No. 2.4e-153;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 53.4%;
Best Local Similarity 99.6%;
Matches 545; Conservative
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ORGANISM
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from mouse cortex. The tag is a string of 5 nucleotides
present between the Not I site and the oligo-dr track.
The library was constructed as described by Bonaldo,
Lennon and Soares, Genome Research 6: 791-806, 1996.
Tissue provided by Ms. Annie Novakovich, Zivic-Miller
Laboratories: "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGACCTTGTGGATGATGTCTTCACTGTCACCGAAGATGAAATCAAGTATGCAACCCAGC 360
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                                                                                                                                                                                                                                                                                                                                   54.4%; Score 554.2; DB 10 99.5%; Pred. No. 1.4e-156;
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BI739030.1 GI:15716056
                                                                                                                                                                                                                                                                                                                                                                       556; Conservative
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house mouse
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Matches 55
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BI738966 823 bp mRNA linear EST 20-SEP-2001 603359780F1 NIH_MGC_94 Mus musculus CDNA clone IMAGE:5367043 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pcMv-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
                                                                                                                                                                                                                                                        301 CCTGCTTACATTGTGGTTCCCCAAACAGCTCCCAACTGCAAGAAACTGGCAATCCAAGCC
                    361 TATGGAGCATCGATAGTATACTGTGACCCAAGTGACGAGTCCAGAGAAAGGTCACTCAA
                                                                                                                                                                                                                                    GCTGGACAAGGAACAATTGCCCTGGAAGTGCTGAACCAGGTTCCCTTGG-TAGATGCACT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1933 row.: p column: 20
High quality sequence stop: 799.
Location/Qualifiers
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Pred. No. 6.2e-134;
0; Mismatches 2; 1
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208 c 193 g 184 t
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/db_xref="taxon:10090"
/clone="IMAGE:5367043"
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Best Local Similarity 98.9
Matches 525; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA sequence.
BI738966
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JOURNAL
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                                                                                                                                                    BQ885621 918 bp mRNA linear EST 16-AUG-2002
AGENCOURT_8754012 NIH_MGC_130 Mus musculus CDNA clone IMAGE:6332599
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14.14.76.4 http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L. Freeman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/db_xref="taxon.10090"
/clone="Inba"NiH_MGC.100"
/lab_host="OH10B (phage-resistant)"
/note="Organ: otcoysts; Vector: pCMV-SPORT6.1.ccdb;
/incl=1: EccRV; Site_2: Not1; Cloned unidirectionally.
/primer: Oligo dT. Average insert size 1.95 kb.
/constructed by ResGen, Invitrogen Corp. Note: this is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: ResGen, Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
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8
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                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 others
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230 c 230
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BQ885621.1 GI:22277639
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|GTGGTAC 819
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Matches 571;
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AUTHORS
TITLE
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KEYWORDS
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 698)
Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okadaraki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Soqabe, Y., Suzuki, H., Muramatsu, Murama
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Fax: 81-298-36-9145
Fax: 81-298-36-9045
Email: genome-res@ttc.riken.go.jp
Carninci.P., Shibata,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Toque,X., Toque,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
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On May 11, 1999 this sequence version replaced
Contact: Chie Owa
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T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into HN Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                               RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
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Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa
,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
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                                                                                                                                                                                                                                                                                                                                           Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to
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On Nov 14, 1999 this sequence version replaced gi:6422138.

Contact: Yoshihide Hayashizaki
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10 (II), 1757-1771 (2000)

11 Compose the sequence of the sequence 
                                                                                                                                                          949 GTAGACCTAAACCTCCCTGAACTGGGTGGGCCAGGCTGAACGGCCCAGCTCCTTACCAGACG 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 24-0CT-2001
                                             URL:http://genome.gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp/
Carninai,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninai,P., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AV374491 G02 bp mRNA linear EST 24-OCT-2003 AV374491 RIKEN full-length enriched, adult male cecum Mus musculus CDNA clone 9130011P22 3', mRNA sequence.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Please visit our web site (http://genome.gsc.riken.go.jp/) for
CATTTCCAAACAGTCTCCCAGAAGTAAAGAACGTCTGCATTGTACTCAGTGGGGGGAAT
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Fax: 81-45-503-9216
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JOURNAL
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prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGCATCTATTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 CIGCIGAGCCCTCGAATGCAGAIGACTGGTACCAGICTAAACTGAAAGGAGAACTGACCC 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 GAATGGTTNCTGGAATANCCATTACAATTAAGGCCCGGAAACCTAGTGTGAAGGTATACG
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                                                                                                                                                                                                              /note="Site_1: SalI; Site_2: BamHI; cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10;
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Pred. No. 2.2e-128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                  /organism="Mus musculus"
                                                                                 /db_xref="taxon:10090"
/clone="9130011P22"
                                                                                                                                                          /tissue_type="cecum"
prepare mouse tissues.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148 g
                                                                                                                                                                            /dev_stage="adult"
/lab_host="DH108"
                                                                  /strain="C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45.38;
94.78;
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mi51e12.yl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:467086 5' similar to SW:YKY8_YEAST P36007 HYPOTHETICAL A1322578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 455)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            420 AGGATGAAACTACTCATTGAACCTACAGCTGGTGTTGGAGTGGCTGCTGTGCTGTCTCAA 479
                                                                                                                                                                                                                                                                                                                                                                                                                    300 GCAGATGGTGTCAAATCCAGCATTGGCTTGAACACCTGGCCTATTATCAGGGACCTTGTG 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   829 AGAATGAAACTGCTCATTGAGCCGACTGCTGGCGTGGCACTGGCTGCTGTGTTCTCAG 888
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                                                                                                                                                                                                  181 GTTAAGGCTCTGAAACCTAGTGTGAAGGTATATGCTGCTGAACCCTCAAATGCAGATGAC
                                                                                                                                                                                                                                                                    649 TGCTACCAGTCTAAACTGAAAGGAGAACTGACCCCCAATCTTCATCCTCCAGAAACCATA
                                                                                                                                                                                                                                                                                                 GCAGATGGTGTCAAATCCAGCATTGGCTTGAATACCTGGCCTATTATAAGAGACCTTGTG
                                                                       GTAGATGCACTGGTACCAGTAGGAGGAGGAGGAATGGTTGCTGGAATAGCCATTACA
                                                                                                                                                                      589 ATTAAGGCCCTGAAACCTAGTGTGAAGGTATACGCTGCTGAGCCCTCGAATGCAGATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GATGATGTCTTCACTGTCACCGAAGATGAAATCAAGTATGCAACCCAGCTGGTGTGGGGG
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Tel: 314 286 1800
Fax: 314 286 1810
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Waterston, R.
The WashU-HHMI Mouse EST Project
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Mammalia; Eutheria;
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Chorozed

Chorozed

Char, Stage="fetal and adult"

(lab_host="DH10B (Life Technologies) (T1 phage resistant)"

//note="Organ: eye; Vector: pt713 Pac (Pharmacia) with a
modified polylinker; Site_1: ECOR I; Site_2: Not I;

UI-E-EJO is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soates, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an ECOR I adaptor, digested
with Not I, and cloned directionally into pT773-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contenins a library tag sequence-that is
located between the Not I site and the (dT)1B tail. The
sequence tags for this library are: fetal eyes AGAATCAAGA;
ilens, CGATTAGCGA; eye anterior segment, AATGCCGCAT;
optic nerve, CCATTAGCGS; retina, CGCGC; Retina Foveal and
Macular, GTCC; RPE and Choroid, ACCTA. This library was
created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI):"
                                           634 bp mRNA linear EST 01-MAR-2002 UI-E-EJO-ahu-j-16-0-UI.rl UI-E-EJO Homo sapiens cDNA clone UI-E-EJO-ahu-j-16-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: msoares@lue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
DNA Sequencing by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
Seq primer: Ml3 Reverses
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata; Craniata; Vertebrata; Buteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                    Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             optic nerve, retina, Retina Foveal and Macular, RPE and Choroid"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/clone="UI-E-EJO-ahu-j-16-0-UI"
/clone_lib="UI-E-EJO"
/tissue_type="fetal eyes, lens, eye anterior segment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             University of Iowa
AST Eckstein Medical Research Building Iowa City,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 45.2%; Score 460.4; DB 14; Length Best Local Similarity 86.7%; Pred. No. 4e-128; Matches 530; Conservative 0; Mismatches 77; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                 Genome Res. 6 (9), 791-806 (1996)
                                                                                                                                                                 BM719814.1 GI:19038647
                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                          discovery
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This read is a RESEQUENCE of a previously sequenced mouse clone This read has been verified (found to hit its original self in the

469 CCTGCAGTGATAGCTGGACAAGGAACAATTGCCCTGGAAGTGCTGAACCAGGTTCCCTTG 528

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Mus musculus
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COMMENT
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                                                                                                                       embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                    Length 455,
                                                                                                                                                  /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
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                                                                                                                                                                                                                                                                                                                                                                                                                  44.7%; Score 455; DB 9; Le
100.0%; Pred. No. 1.4e-126;
iive 0; Mismatches 0;
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/clone_lib="Soares mouse
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Seq primer: -40RP from Gibco
High quality sequence stop: 4
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           M.Fatima Bonaldo
                                                                                                                                    /sex="unknown'
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 455; Conserv
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Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:10090"
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/clone="ImAGE:4985337"
/clone="in="Nor:GAA_CO24"
/lab_host="bH10B (Tl phage-resistant)"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 163 c 174 g 181 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 729)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLAMA0992 row: l column: 06
High quality sequence stop: 719.
Location/Qualifiers
                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Pred. No. 1.4e-123;
0; Mismatches 4; 1
                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="FVB/N"
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Best Local Similarity 98.9%;
Matches 459; Conservative
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Search completed: June 24, 2003, 05:35:27

BG965678 11near EST 12-JUN-2001 602830522F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4985237 5',

GI:14353315

mRNA sequence. BG965678 BG965678.1 GI:

> ACCESSION VERSION

DEFINITION

rocus

Tue Jun 24 15:38:55 2003

Job time : 1468 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

June 24, 2003, 05:36:57; Search time 19.4713 Seconds (without alignments) 722.114 Million cell updates/sec Run on:

US-09-889-609B-8 1740 1 MCAQYCISFADVEKAHINIQ.....TSLNWVGQAERPAPYQTVSV 339 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Query Match Length DB
Query Match Length DB
90.0 340 1 33.7 226 1
33.7
28.2 329 1
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36 25.1 332 1
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20.9 422 1
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30 mycobacteri	33 synechocyst	17 flavobacter	e3 bacillus ha	20 homo sapien	98 arabidopsis	33 brassica ju	17 citrullus 1	28 campylobact	32 rattus norv	35 brassica ju	
P95230	F/413	0594	09k7e	P355	P479	0237	0433	P711:	P322	0237	Q9xea8
CYSK_MYCTU	THRC_SYNY3	CYSK_FLASP	THRC_BACHD	CBS_HUMAN	CYSK_ARATH	CYK1_BRAJU	CYSK_CITLA	CYSM_CAMJE	CBS_RAT	CYK2_BRAJU	CYK2_ORYSA
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11.4 31			10.8	10.7	10.4	10.2	10.2	10.1	10.1	6.6	6.6
	11.4	10.9			• •		, ,				

ALIGNMENTS

1 MCAQYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGA 60

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STRAIN=S288c
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P36007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MCAQYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGA
                     LNAIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQA
                                 YGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDAL
                                                                                                         VVPVGGGGWVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGV
                                                                                                                                                  KSSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQT
                                                                                                                                                             DeMiranda J., Santoro A., Engelender S., Wolosker H.;
"Human serine racemase: molecular cloning, genomic organization and
functional expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY
                                                                                                                                                                                                                                                                                                                                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                           VSPEVKNVCIVLSGGNVDLTSLNWVGQAERPAPYQTVSV 339
                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine racemase (EC 5.1.1.-).
                                                                                                                                                                                                                                                                        AA
                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Brain;
MEDLINE-20510003; PubMed-11054547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF169974; AAG27081.1; -. EMBL; AK023169; BAB14442.1; -.
                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     functional expression.
Gene 256:183-188(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                    SRR_HUMAN
Q9GZT4;
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Genew; HGNC:14398; SRR.

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                                                                                                                                                                                                                                                                      1 MCAQYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGA
                                                                                                                                                                                                                                                                                                                              61 LNAIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQA
                                                                                                                                                                                                                                                                                                                                                                                                              YGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGGGTIALEVLNQVPLVDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241 KSSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                             SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryotas Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
                                                                                                                                                                                                             ij
                                                                                                                                                                     340;
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"The complete sequencing of a 24.6 kb segment of yeast chromidentified the known loci URA1, SAC1 and TRP3, and revealed open reading frames including homologues to the threonine dehydratases, membrane transporters, hydantoinases and the phospholipase A2-activating protein.";
                                                                                                                                                                       Length
                                                                                                                                                                                                             Indels
                                                                   PROSITE; PSUGLOU, CONTROL PHOSPHATE (BY SI
ISOMERASE; PYLIDOXAL PHOSPHATE (BY SI
BINDING 56 56 PYRIDOXAL PHOSPHATE (BY SI
AND AND 36566 MW; 873342C62D5D7B9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 34.9 kba protein in COS9-JENI intergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339
                                                                                                                                                             90.9%; Score 1582.5; DB 1;
89.7%; Pred. No. 7.2e-114;
tive 19; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSPEVKNVCIVLSGGNVDLT-SLNWVGQAERPAPYQTVSV
                                                              PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
InterPro; IPR001926; B6_enzyme_beta
InterPro; IPR000634; S/T_dehydrtse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95028164; PubMed=7941750;
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                            Pfam; PF00291; PALP; 1
                                                                                                                                                                                      Similarity
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THD2_SALTY
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                                                                                                                                                                                                                                                                                                                                                              247 NTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 IPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVY 127
                                                                                                                                                                                                                                          67
                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S., Browns K., Brown D., Brown S., Chillingworth T., Churcher C. M., Collins M., Connor R., Croin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Honsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Oliver K., O'Neil S., Pearson D., Quail M.A., Rabbinowitsch E., Rutherford K., Ruther S., Saunders D., Seeger K., Sharp S., Skelton J., Simmonds M., Squares R., Squares S., Stevens K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
                                                                                                                                                                                                                                                                                                                                                                                                                8 SFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGL
                                                                                                                                                                                                                                                       GMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSS-IGL
                                                                                                                 PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Hypothetical protein; Lyase; Pyridoxal phosphate.
BINDING 53 53 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                               8;
                                                                                                                                                                                   33.7%; Score 587; DB 1; Length 326; 40.9%; Pred. No. 8.8e-38;
                                                                                                                                                                                                               66; Mismatches 111; Indels
                                                                                                                                                          21CF7FEFC8AB4431 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein G320.14 in chromosome III.
SPCG320.14 OR SPCG330.15C.
Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 AA.
                                                              SGD; SO001701; YKL218C.
InterPro; IPR0001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
Pfam; PF00291; PALP; 1.
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                                                                                                                                                          326 AA; 34899 MW;
EMBL; X75951; CAA53555.1; -. EMBL; Z28218; CAA82063.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | |:||||||:
298 KVGIILSGGNVDM 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 NVCIVLSGGNVDL 319
                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                       PIR; S38061; S38061.
PIR; S44320; S44320.
HSSP; P04968; 1TDJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
                                                                                                                                                                                                 Best Local Similarity
Matches 128; Conserv
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SEQUENCE FROM N.A.
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                                                                                                                                                         SEQUENCE
                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 IPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69 ---NEAQRKAGVLTFSSGNHAQAIALSAKILGIPAKIIMPLDAPEAKVAATKGYGGQVIM 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDPSDESREKVTQRIMQETEGI-LVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGG 186
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                      Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H., Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., Eger P., Zimmermann W., Weller H., Wambutt R., Purnelle B., Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M., Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G., Daga R.R., Cruzado L., Jimmenz J., Sanchez M., dailardin C., Eucher M., Galibert B., Moreno S., Armstrong J., Forsburg S.L., Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J., Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1989 (Rel. 12, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase catabolic (EC 4.2.1.16) (Threonine deaminase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 415:871-880(2002).
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PYRIDOXAL PHOSPHATE (BY SIMILARITY). 21187E5A69FA5348 CRC64;
Robben J., Grymonprez B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Pred. No. 1e-35;
68; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FALSE_NEG.
phosphate.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.2%; Score 560; 39.6%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00165; DEHYDRATASE_SER_THR; Hypochetical protein; Lyase; Pyridoxal BINDING 57 57 PRIDOXAL SEQUENCE 323 AA; 35048 MW; 21187E5A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL, AL022245; CAA18316.1; -.
EMBL, AL031603; CAA20920.1; -.
HSSP, P04966; 1TPD.
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR001936; S/T_dehydrtse.
Pfam: PF00291; PALP; 1.
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KNKRIGIIISGGNVDI 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 39.69
Matches 125; Conservative
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303 NRKTVS-----IISGGNIDLSRVSQ1 323
                                                                                                       297 HFQTVSPEVKNVCIVLSGGNVDLTSLNWV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=0157:H7 / EDL933 / ATCC 700927;
MEDLINE=21074935; PubMed=11206551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic Acids Res. 17:3994-3994(1989)
                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-0157:H7 / RIMD 0509952;
MEDLINE-21156231; PubMed-11258796;
                                                                                                                                                                                                                                                                                          TDCB OR B3117 OR Z4469 OR ECS3997
Escherichía coli, and
                                                                                                                                                                                                                                01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last seq
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                      Escherichia coli 0157:H7.
                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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ID THD2_ECOLI
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                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L---TEAEKRKGVVACSAGNHAQGVSLSCAMLGIDGKVVMPKGAPKSKVAATCDYSAEVV 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 -YCDPSDESREKVTQRIMQETEG-ILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRG 66
                                                                                                                                                                                                                                                                                                                                                                                     ENZYME REGULATION: EACH PROTEIN MOLECULE CAN BIND UP TO FOUR MOLECULES OF AMP, WHICH ACTS AS AN ALLOSTERIC ACTIVATOR TO THE ENZYME. THE ENZYME IS ALSO INHIBITED BY ALPHA-KETO ACIDS AND OTHER CATABOLITES. IT IS ALLOSTERICALLY INHIBITED BY ISOLEUCINE AND ALLOSTERICALLY ACTIVATED BY VALINE.
                                                                                                             MEDLINE-21534948; PubMed-11677609; McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Materston R., Wilson R.K.; "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185 GGGGWVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SS
                                                                                                                                                                                                                                                                                                                  from two enteric bacteria.";
Biochim. Biophys. Acta 706:27-35(1982)
-!- CATALYTIC ACTIVITY: L-threonine + H(2)O = 2-oxobutanoate + NH(3)
                                                                                                                                                                                                                                                                                                    characterization of biodegradative threonine dehydratases
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PATHWAY: Threonine catabolism.
SUBUNIT: HOMOTETRAMER.
SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interrio; Atheria of Palp, 1.
Prosite; PS00165; DEHYDRATASE_SER_THR; 1.
Lyase; Pyridoxal phosphate; Allosteric enzyme; Complete proteome.
Pyridoxal phosphate; Pyridoxal PHOSPHATE (BY SIMILARITY)
TDCB OR STM3244.
Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K -> I (IN REF. 2).
C1C619B021DE817C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.2%; Score 491; DB 1; Le
36.8%; Pred. No. 2e-30;
Live 68; Mismatches 116;
                                                                                                    STRAIN-LT2 / SGSC1412 / ATCC 700720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Interpro; IPR001926; B6_enzyme_beta.
Interpro; IPR000634; S/T_dehydrtse.
                                                                                                                                                                                                                                                                                                                                                                         -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- ENZYME REGULATION: FACH PROTEI
                                                                                                                                                                                                                                                          SEQUENCE OF 1-24.
MEDLINE-83023208; PubMed=6751404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE008849; AAL22117.1; -.
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                                                                                                                                                                                                                                Nature 413:852-856(2001).
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StyGene; SG10390; tdcB.
                                                                                                                                                                                                                                                                                     Kim S.S., Datta P.; "Chemical character
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                   SEQUENCE FROM N.A.
                                                        NCBI_TaxID=602;
                                           Salmonella,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121;
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Matches
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243 PGNLTYEIVRELVDDIVLVSEDEIRNSMIALIQRNKVITEGAGALACAALLSGKLDSHIQ
IGLNTWP11RDLVDDVFTVTEDE1KYATQLVWGRMKLLIEPTAGVALAAVLS-----Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1988 (Rel. 09, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase catabolic (EC 4.2.1.16) (Threonine deaminase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-K12 / W3110;
MDELINE-89282418; Pubmed-2660107;
Schweizer H., Datta P.;
"The complete nucleotide sequence of the tdc region of Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., "Welch R.A., Blattner F.R.; "Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7."; Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRAIN=K12 / W3110;

MEDLINE=87092415; PubMed=3540965;

Datta P., Goss T.J., Omnasa J.R., Patil R.V.;

"Covalent structure of biodegradative threonine dehydratase of Escherichia coli: homology with other dehydratases.";

Proc. Natl. Acad. Sci. U.S.A. 84:393-397(1987).
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                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 PGNLTYEIVRELVDDIVLVSEDEIRNSMIALIQRNKVVTEGAGALACAALLSGKLDQYIQ 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -YCDPSDESREKVTQRIMQETEG-ILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPV 184
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                                                                                                                                                                                          ENZYME REGULATION: EACH PROTEIN MOLECULE CAN BIND UP TO FOUR MOLECULES OF AMP, WHICH ACTS AS AN ALLOSTBRIC ACTIVATOR TO THE ENZYME. THE ENZYME IS ALSO INHIBITED BY ALPHA-KETO ACIDS AND OTHER CATABOLITES. IT IS ALLOSTBRICALLY INHIBITED BY ISOLEUCINE AND ALLOSTBRICALLY ACTIVATED BY VALINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGGWVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SS
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                                                                                                                                                                                                                                                                                          -i- INDUCTION: TRANSCRIBED IN RICH MEDIUM. IT IS MADE ANAEROBICALLY.
-i- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                      -!- CATALYTIC ACTIVITY: L-threonine + H(2)0 = 2-oxobutanoate + NH(3)
                                                                     Kim.S.S., Datta P.;
"Chemical characterization of biodegradative threonine dehydratases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
comparison with a laboratory strain K-12.";
                                                                                              from two enteric bacteria.";
Biochim. Biophys. Acta 706:27-35(1982).
-!- FUNCTION: ACTS ON BOTH SERINE AND THREONINE, AND PROPERLY CONSIDERED AS A HYDROXY AMINO ACID DERMINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 AA; 35232 MW; E7DF018FCCF743B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27.4%; Score 476; DB 1;
35.9%; Pred. No. 2.7e-29;
iive 70; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lyase; Pyridoxal phosphate; Allosteric enzyme;
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InterPro; IPR000634; S/T_dehydrtse.
                                                                                                                                                                                                                                                                PATHWAY: Threonine catabolism. SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                -!- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                       PubMed=6751404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, M23638; AAA24661.1; -.
EMBL, U18997; AAA57921.1; -.
EMBL, AE000393; AAC76152.1; -.
EMBL, AE005540; AAG58248.1; -.
EMBL, AP002564; BAB37420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M21312; AAA24660.1; -. EMBL; X14430; CAA32593.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 118; Conservative
 nd genomic com
8:11-22(2001).
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P04968; 1TDJ
                                          SEQUENCE OF 1-25.
MEDLINE=83023208;
 and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Molecular basis of symbiosis between Rhizobium and legumes.";
Nature 387:394-401(1997).
-!- CATALYTIC ACTIVITY: L-threonine + H(2)O = 2-oxobutanoate + NH(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative threonine dehydratase (EC 4.2.1.16) (Threonine deaminase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- PATHWAY: Isoleucine biosynthesis; first step.
-i- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
BUT LACK THE C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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Best Local Similarity 32.6%; Pred. No. 3.2e-26;
Matches 105; Conservative 70; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRIDOXAL PHOSPHATE.
A46DE121CC33519F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00291; PALP; 1.
PROSTIE; PS00165; DEWFYDRATASE_SER_THR; 1.
HYPOTHELICAL protein; Isoleucine biosynthesis; Lyase; Pyridoxal phosphate; Plasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                        332 AA
                                                            303 NRKTVS-----IISGGNIDLSRVSQI 323
297 HFQTVSPEVKNVCIVLSGGNVDLTSLNWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=97305956; PubMed=9163424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000098; AAB91863.1; -.
                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhizobium sp. (strain NGR234).
Plasmid sym pNGR234a.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=394;
                                                                                                                                                                                                                  Y4TJ_RHISN
P55664;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perret X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29
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HI0738.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter J.C.;
                                                                                                                                                                                                                   THD1_HAEIN
                                                                                                                                                                                                                                                                                deaminase)
                                                                                                257
                                                                                                                     259
                                                                                                                                                                                                                           P46493
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TIGR;
                                                                                                                                                                                                        THD1_HAEIN
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                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as 'long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
241 KSSIGL-NTW--PIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQH 297
               19 IQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 VYDVAQVTPLQDMAKLSERLGNKVFIKREDRQPVHSFKLRGAYAMIAGL---SAEQKASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 VVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPS-DESREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                  -:- PATHWAY: Isoleucine biosynthesis; first step.
-:- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-:- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                               Bacteria, Proteobacteria, gamma subdivision, Pasteurellaceae,
Pasteurella.
                                                                                                                                    15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase biosynthetic (EC 4.2.1.16) (Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.2%; Score 421; DB 1; Length 51 34.1%; Pred. No. 7.7e-25; ive 63; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3E427ADC54E5FC7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGRO1124; ilva_2Cterm; 1.
PROSITE; PSO0165; DEHYDRATASE_SER_THR; 1.
Isoleucine blosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                              H(2)O.
-!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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                                                                                                                  513 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
InterPro; IPR001721; ThrDh_C.
Pfam; PF00291; PALP; 1.
                                                      -GKVAARGGSVGVVLSGQNIDM 315
                                        298 FQTVSPEVKNVCIVLSGGNVDL 319
                                                                                                                                                                                                                                                                              MEDLINE=21145866; PubMed=11248100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00585; Thr_dehydrat_C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56288 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE006199; AAK03708.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                  STANDARD;
                                                                                                                                                                                                      Pasteurella multocida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          513 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome.
                                                                                                                                                                                                                                   NCBI_TaxID=747;
                                                                                                                                                                                           ILVA OR PM1624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P04968;
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                                                                                                                  THD1_PASMU
                                                                                                                                                                                deaminase)
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                                              DDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVKNVCIVLSGGN 316
138 VTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMVAGIAITI 197
                                                                                                                                                                                                                                              KQLMPEIKVIGVE-SKDSACLYRALKAGKPIDLDRVGLFADGVAVKRIGDETFRVCQQYI 258
                                                                                                                                                                 KALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SSIGLNTWPIIRDLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Koonin E.V., Rudd K.E.;
Submitted (SEP-1995) to the SWISS-PROT data bank.
-!- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
threonine in a two-step reaction. The first step is a dehydration
of threonine, followed by rehydration and liberation of ammonia.
-!- CATALYTIC ACTIVITY: L-threonine + H(2)O = 2-oxobutanoate + NH(3) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Rd / KW20 / ATCC 51907;

MEDLINE=95330630; PubMed=7542800;

Rellavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., Mcrischmen K. D., Sult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fielde C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Uttenback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1995 (Rel. 32, Created)
U-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase biosynthetic (EC 4.2.1.16) (Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- COFÁCTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
-!- PATHWAY: Isoleucine biosynthesis: first step.
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          513 AA
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LNFHTLRYVSE 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             317 VDLTSLNWVGQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel.
01-NOV-1995 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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IDENTIFICATION
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CATALYTIC ACTIVITY: L-threonine + H(2)0 = 2-oxobutanoate + NH(3)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MITOCHONDRION (POTENTIAL)
THREONINE DEHYDRATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        I -> T (IN REF. 1).
0801BCBD7EEDDC1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68; Mismatches 131;
                                                     COFACTOR: PYRIDOXAL PHOSPHATE.
ENZYME REGULATION: ISOLEUCINE ALLOSTERICALLY
VALINE ALLOSTERICALLY ACTIVATES THIS ENZYME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRIDOXAL PHOSPHATE.
                                                                                                                        PATHWAY: Isoleucine biosynthesis; first step. SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.7%; Score 395.5; DB 1 32.5%; Pred. No. 7.9e-23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transit peptide; Allosteric enzyme.
TRANSIT 1 ? MITOCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 YVPILSGANMNFDRLRFVSE 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CI-VLSGGNVDLTSLNWVGQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63831 MW;
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Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109
259
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259
576 AA;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72 PEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGIAITIKALKPSVKVYAAEPSNADDCYQSKL-KGELTPNLHPPETIADGVK-SSIGLNT 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVKNV 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 VEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDT 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Nucleotide sequence of the gene for threonine deaminase (ILV1) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-S288C / AB972;

STRAIN-S288C / AB972;

Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Cherry Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Wosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase, mitochondrial precursor (EC 4.2.1.16)
                                                                                                                                                                                                                                                                              23.3%; Score 405; DB 1; Length 513; 32.6%; Pred. No. 1.3e-23; ive 68; Mismatches 137; Indels
                                                                                                                                                                                                                PYRIDOXAL PHOSPHATE.
DF42CA8B6FDE4CD7 CRC64;
                                                                   Pfam; PF00291; PALP; 1.
Pfam; PF00291; PALP; 1.
Pfam; PF00185; Thr_dehydrat_C: 2.
TIGRFAMs; TIGRO1124; ilvA_2Cterm; 1.
PF051TE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Kielland-Brandt M.C., Holmberg S., Petersen J.G.L.,
Nilsson-Tillgren T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 576 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carlsberg Res. Commun. 49:567-575(1984).
IPR001926; B6_enzyme_beta.
IPR000634; S/T_dehydrtse.
IPR001721; ThrDh_C.
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312 AAILSGANLNFHTLRYVSE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CIVLSGGNVDLTSLNWVGQ 327
                                                                                                                                                                                                                                     56662 MW;
                                                                                                                                                                                                                                                                                                                               Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae.
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                                                                                                                                                                                                                                   SEQUENCE 513 AA;
                                                                                                                                                                                            Complete proteome.
                                                                                                                                                                                                                                                                                                         Similarity
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                                                  InterPro;
                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV-YCDPSDESRE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KVTQRIMQETEGIL-VHPNQEPAVIAGQGTIALEVLNQVPL---VDALVVPVGGGGMVAG 192
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                                                                                                                                                                                                                                                                                                                                                   EMBL; M36383; AAA34705.1; -.

R EMBL; X01466; CAA25696.1; -.

R EMBL; X01466; CAA25696.1; -.

R EMBL; U18839; AAA644641.1; -.

R PIR; A01150; DWAPT.

R HSSP; P04968; 1TDJ.

R GCD; S0000888; 1LVJ.

R INTERPRO; IPR001926; B6_enzyme_beta.

R InterPro; IPR001921; ThrDh_c.

R InterPro; IPR001721; ThrDh_c.

R Ffam; PF00391; PALP; 1.

R TIGREAMS; TIGRO1124; ilvA_2Cterm; 1.

R TIGREAMS; TIGRO1124; ilvA_2Cterm; 1.

R SOSITE; PS00165; DEHYDRATASE_SER_THR; 1.

W RSOSITE; PS00165; DHYDRATASE_SER_THR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Mitochondrial.
SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
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ID THD1_SALTY STANDARD; F
AC P20506; 091688;
DT 01-FEB-1991 (Rel. 17, Created)
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                                                                                                                                                                                                                                                                                                                                   STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINEx-15S4948; Pubmed=11677609;
MCCLelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nauyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: Catalyzes the formation of alpha-ketobutyrate from threonine in a two-step reaction. The first step is a dehydration of threonine, followed by rehydration and liberation of ammonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COPACTOR: PYRIDOXAL PHOSPHATE.
-!- ENZYME REGULATION: ISOLEUCINE ALLOSTERICALLY INHIBITS WHEREAS VALINE ALLOSTERACALLY ACTIVATES THIS ENZYME.
-!- PATHANY: ISOleucine biosynthesis; first step.
-!- SUBUNIT: HOMOTETRAMER.
-!- SUBUNIT: HOMOTETRAMER.
                                                                                 Salmonella typhimurium.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                            SEQUENCE FROM N.A. MEDLINE-8825570; PubMed=3290055; MEDLINE-8825570; PubMed=3290055; Taillon B.E., Little R., Lawther R.P.; Analysis of the functional domains of biosynthetic threonine deaminase by comparison of the amino acid sequences of three wild type alleles to the amino acid sequence of biodegradative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lopes J.M., Lawther R.P.; "Physical identification of an internal promoter, ilvAp, in the distal portion of the ilvGMEDA operon.";
                 15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase biosynthetic (EC 4.2.1.16) (Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;
15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; it.....
Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C; 2.
TIGREAMS; TIGRO1124; ilvA_2Cterm; 1.
TIGREAMS; TIGRO1124; ilvA_2Cterm; 1.
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Interpro; IPR000634; S/T_dehydrtse.
Interpro; IPR001721; Thrbh_C.
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                                                              ILVA OR STM3905 OR STMD1.87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-10 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 413:852-856(2001).
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StyGene; SG10179; i
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                                                                                                                                NCBI_TaxID=602;
                                                                                                                  Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                  138 VTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMVAGIAITI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                          KALKPSVKVYAAEPSNADD--CYQSKLKGELTPNLHPPETIADGVK-SSIGLNTWPIIRD 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||: || | | | : :: :: ||: :||| : :: |
258 YLDDIIITVDSDAICAAMKDLFEDVRAVAEPSGALALAGMKKYIAQH----NIRGERLAHV 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          201 KQLMPQIKVIAVE---AEDSACLKAALEAGHPVDLPRVGLFAEGVAVKRIGDETFRLCQE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAV---LSQHFQTVSPEVKNVCIV 311
                                                                                                                                                                                                                                      19 IQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPKA 78
                                                                                                                                                                                                                                                         Wartmann T., Roesel H., Kunze I., Bode R., Kunze G.;
"ALIVI gene from the yeast Arxula adeninivorans LS3 -- a new selective transformation marker.";
Yeast 14:1017-1025(1998).
-!- CATALYTIC ACTIVITY: L-threonine + H(2)O = 2-oxobutanoate + NH(3)
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: Isoleucine biosynthesis; first step.
SUBUNIT: HOMOTETRAME (BY SIMILARITY).
SUBCELLULAR LOCATION: Mitochondrial.
SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodascaceae; mitosporic Dipodascaceae; Arxula.
                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase, mitochondrial precursor (EC 4.2.1.16)
                                                                                                                                                              ; DB 1; Length 514; 5.2e-22;
                                                                                                                                                                                                  69; Mismatches 127; Indels
                                  A -> T (IN REF. 1).
F -> L (IN REF. 1).
A -> G (IN REF. 1).
A -> T (IN REF. 1).
SFL -> NFP (IN REF. 1).
                  PHOSPHATE
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                                                                                                                                                              22.1%; Score 384; 32.3%; Pred. No. 5
   proteome.
PYRIDOXAL
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                                                                                                                            56253 MW;
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   Complete
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                  62
71
124
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                                                                                                                          514 AA;
                                                                                                                                                                                 Similarity
     enzyme;
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124
339
342
351
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Allosteric
BINDING
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EMBL;
 (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                     78 AVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPSDESREK 137
                                                                                                                                                                                                                                                                                                                       195 ITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSSI-GLNTWPIIR 253
                                                                                                                                                                                                                                                                                                                                                           DLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEV----KNVC 309
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                                                                                                                                                                                                           19 IQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEE-KPK 77
                                                                                                                                                                                                                                                                                               TIGREAMS; TIGR01124; ilvA_2Cterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Mitochondrion; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                       21.8%; Score 379.5; DB 1; Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-88056322; PubMed-3315862;
COX J.L., COX B.J., Fidanza V., Calhoun D.H.;
"The complete nucleotide sequence of the ilvGMEDA cluster of
Escherichia coli K.12.";
Gene 56:185-198(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-AUG-1987 (Rel. 05, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase biosynthetic (EC 4.2.1.16) (Threonine
                                                                                                                                                                                          Indels
                                                                                                                           MITOCHONDRION (POTENTIAL). THREONINE DEHYDRATASE.
                                                                                                                                                     DOSCESBD55CC8A6F CRC64;
                                                                                                                                                                                          56; Mismatches 139;
                                                                                                                                              PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                 Pred. No. 1.2e-21;
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tities requires a license agreement (S send an email to license@isb-sib.ch).
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Garrison E., Harms E., Umbarger H.E.;
                                         Interpro: IPR001926; B6_enzyme_beta.
Interpro: IPR001934; S/T_dehydrtse.
Interpro: IPR001013; ThrDh_C.
Pfam: PF00291; PALP; 1.
Pfam: PF00585; Thr_dehydrat_C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                               341 AILSGANMDFDRLRFVSE 358
                                                                                                                                                     550 AA; 60416 MW;
                         EMBL, AJ222772; CAA10977.1; -. HSSP; P04968; 1TDJ.
                                                                                                                                                                                          Conservative
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                                                                                                                                   550
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es 106; Conserv
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SEQUENCE FROM N.A.
STRAIN=K12;
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NCBI_TaxID=562;
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ILVA OR B3772.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
MEDLINE=98230745; PubMed=956256;
Gallagher D.T., Gilliland G.L., Xiao G., Zondlo J., Fisher K.E.,
Chinchilla D., Eisenstein E.;
"Structure and control of pyridoxal phosphate dependent allosteric
threonine deaminase.";
Structure 6:465-475(1998).
-:- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from
threonine in a two-step reaction. The first step is a dehydration
of threonine, followed by rehydration and liberation of ammonia.
Deaminates L-threonine, but also L-serine to a lesser extent.
-:- CATALYTIC ACTIVITY: L-threonine + H(2)O = 2-oxobutanoate + NH(3) +
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=KIZ / MG165;
STRAIN=KIZ / MG1655;
BMEDINE-9335824; PubMed-1379743;
Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
"Analysis of the Escherichia coli genome: DNA sequence of the region Science 257:771-778(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- ENZYME REGULATION: ISOLEUCINE ALLOSTERICALLY INHIBITS WHEREAS VALUNE ALLOSTERICALLY ACTIVATES THIS ENZYME.
-!- PATHRAY: ISOLeucine biosynthesis; first step.
-!- SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=86111952; PubMed=3003115;
Wek R.C., Hatfield G.W.;
"Nucleotide sequence and in vivo expression of the ilvy and ilvC
genes in Escherichia coli K12. Transcription from divergent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lopes J.M., Lawther R.P.; "Physical identification of an internal promoter, ilvAp, in the distal portion of the ilvGMEDA operon."; Gene 76:255-269(198)
                                                                                                                                                                                        E.
                                                                                                                                                                                                                                                            'The complete nucleotide sequence of the ilvGMEDA operon of
Submitted (AUG-1986) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                    MEDLINE-87174741; Pubmed-3550695;
Lawther R.P., Wek R.C., Lopes J.M., Pereira R., Taillon
Hatfield G.W.;
                                                                                                                                                                                                                                                                                                    Escherichia coli K-12.";
Nucleic Acids Res. 15:2137-2155(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     overlapping promoters."; .
J. Biol. Chem. 261:2441-2450(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12;
MEDLINE=89326124; PubMed=2473940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [5]
SEQUENCE OF 439-514 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X04890; CAA28577.1; -. EMBL; K03503; AAA24014.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, K03503; AAA24014.1; -. EMBL, M10313; AAB59054.1; -. EMBL, M11689; AAA24027.1; -. EMBL, M32253; AAA24024.1; -. EMBL; M87049; AAA67575.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE000453; AAC77492.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-10 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M25497; AAA24015.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; B27310; DWECTS
                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 QYLVDILASPVYDVAIESPLELAEKLSDRL-----GVNFYIKREDKQRVFSFKLRGAYNM 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 -SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQ-HFQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 SIV-YCDPSDEŞREKVTQRIMQETEGI-LVHPNQEPAVIAGQGTIALEVLNQVPLVDALV 181
                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         266 IPVGGGGLIAGVATFFKQIAPNTKIIGVEPYGAASMTLSLHEGHRV-KLSNVDFFADGVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 IRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 VPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 QYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNA
                      CATALYTIC ACTIVITY: L-threonine + H(2)0 = 2-oxobutanoate + NH(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY
                                                                                                        -!- PATHWAY: Isoleucine biosynthesis; first step.
-: SUBUNT: HOWOTETRAMER.
-!- SUBCELLULAR LOCATION: Chloroplast
-!- MISCELLANEOUS: EXPRESSION IN MATURE FLOWERS IS INCREASED OVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGREAMS; TIGRO1124; ilva_2Cterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Chloroplast; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THREONINE DEHYDRATASE BIOSYNTHETIC.
PYRIDOXAL PHOSPHATE (BY SIMILARITY)
64937 MW; AC430BB5DD9F0348 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17;
                                                                                    ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY ISOLEUCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          595;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                      the Swiss Institute of Bioinformatics and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  146;
88:2678-2682(1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THD1_ARATH STANDARD; PRT; 592 ÀA Q92SSG; Q95PF1; Created) 15-JUN-2002 (Rel. 41, Created) 15-JUN-2002 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.4%; Score 371.5; 31.3%; Pred. No. 5.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        300 TVSPEVKNVCIVLSGGNVDLTSLNWV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
InterPro; IPR001721; ThrDh_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                385 KIKNE--NIVAIASGANMDFSKLHKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Allosteric enzyme; Transit peptide
                                                                  COFACTOR: PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001721; ThrDh_C.
Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M61914; AAA34171.1; -. EMBL; M61915; AAA68097.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A38628; A38628
HSSP; P04968; 1TDJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPS-DESREK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 IQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPKA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KALKPSVKVYAAEPSNADD -- CYQSKLKGELTPNLHPPETIADGVK - SSIGLNTWPIIRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVKNVCIVLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lycopersicon esculentum (Tomato).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase biosynthetic, chloroplast precursor (EC 4.2.1.16) (Threonine deaminase) (TD)
                                                                                                                                                                                                                                                                                                                                                                                                                                9D389A0EDD8DE692 CRC64;
                                                                                                                                                                                      Pram; Process; Thr_dehydrat_C; 2.
TIGRFAMS; TIGR01124; ilvA_2Cterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Pyridoxal phosphate; Allosteric enzyme; 3D-structure; Complete proteome.
BINDING 62 62 PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67; Mismatches 134;
                                                                                                                                                                                                                                                                                                                       A -> R (IN REF. 2).
A -> R (IN REF. 2).
G -> C (IN REF. 3).
G -> V (IN REF. 3).
G -> V (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.7%; Score 378; DB 1; 31.9%; Pred. No. 1.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       structure, and upregulation in floral organs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             595 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 52-61.
                                                                                                      InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
InterPro; IPR001721; ThrDh_C.
Pfam: PF00291; PALP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. TINY TIM LA154;
MEDLINE=91187855; Pubmed=2011578;
                                        PDB; 1TDJ; 18-NOV-98.
ECO2DBASE; F050.1; 6TH EDITION.
EcoGene; EG10493; ilvA.
                                                                                                                                                                                                                                                                                                                                                                                                                                  56195 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||: | :| :| ANVNFHGLRYVSE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNVDLTSLNWVGQ 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  514 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 100; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             THD1_LYCES P25306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                             CONFLICT
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Best Loca Matches

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241

THD1_LYCES

antimetabolite L-O-methylthreonine

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RA MEDILIDE_ZIOLO/ZO: FUNDMEGE_IIIJO/LO:
RA MEDILIDE_ZIOLO/ZO: FUNDMEGE_IIIJO/LO:
RA Patrmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Ra Delseny M., Grivell L.A., Mache R., Pulgdomenech P.,
RA De Simone V., Choisne N., Artiguenave F., Robert C., Eucottier P.,
RA Mincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Windelmann R., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Windelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Wezzil A., D'Angelo M., Pallavicini A., Toppo S., Simionati B.,
RA Navarro P., Collado M., Pallavicini A., Toppo S., Simionati B.,
RA Navarro P., Collado C., Perez-Perez A., Ottenweatder B., Duchemin D.,
RA Navarro P., Callado C., Perez-Perez A., Ottenweatder B., Masuy D.,
Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Monfort A., Argition A., Flores M., Liguori R., Vitale D.,
Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Otterback T., Fujii C.Y., Shea T.P.,
RA Preuss D., Lin X., Nermann W.C., Salzberg S.L., White O., Venter J.C.,
RA Preuss D., Lin X., Nermann W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C. M., Kaneko T., Nermann W.C., Salzberg S.L., White O., Venter J.C.,
RA Sasamoto S., Kimura T., Idesawa K., Kawashima K., Kishida Y.,
Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
Ratanabe A., Yamada M., Yasuda M., Tabata S.;
RT Sequence and analysis of chromosome 3 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: L-threonine + H(2)0 = 2-oxobutanoate + NH(3) +
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase biosynthetic, chloroplast precursor
(EC 4.2.1) (Threonine deaminase) (TD).
OMRI OR AT3G10050 OR T22XIB.12.
Arabidopsis thallana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudioctyledons; core eudiccts; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 408:820-822(2000).
-!- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from threonine in a two-step reaction. The first step is a dehydration of threonine, followed by rehydration and liberation of ammonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
ENZYME REGULATION: Allosterically inhibited by isoleucine. Strain
GM11b is isoleucine feedback insensitive and is resistant to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mourad G., Emerick R., Smith A.;
"Molecular cloning and sequencing of a cDNA encoding an isoleucine feedback insensitive threonine dehydratase/deaminase of Arabidopsis thaliana line GM11b.";
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=CV. Columbia;
Mourad G., Emerican A., Smith A.;
Mourad G., Emerican G., Employers thaliana.";
[1] Plant Gene Register PGR98-199.
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mourad G.S., Smith A.M.; "Molecular characterization of the genomic clone, including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                promoter sequences, of threonine dehydratase/deaminase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (In) Plant Gene Register PGR00-020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. GM11b;
MEDLINE=20144028; PubMed=10677454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-cv. Columbia;
MEDLINE-21016720; PubMed-11130713;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 SIV-YCDPSDESREKVTQRIMQETEGI-LVHPNQEPAVIAGQGTIALEVLNQV--PLVDA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 LVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETI--- 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ADGVK-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVAL 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MVKLPAD----QLAKGVICSSAGNHAQGVALSASKLGCTAVIVMPVTTPEIKWQAVENLGA
             PATHWAY: Isoleucine biosynthesis; first step.
SUBCELLULAR LOCATION: Chloroplast (By similarity).
SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGR01124; ilva_27term; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Chloroplast; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHLOROPLAST (POTENTIAL).
THREONINE DEHYDRATASE BIOSYNTHETIC.
PYRIDOXAL PHOSPHATE (BY SIMILARITY).
R -> C (IN STRAIN GM11B).
R -> H (IN STRAIN GM11B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.3%; Score 371; DB 1; Length 592; 31.6%; Pred. No. 6.1e-21; ive 61; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAVLSQHFQTVSPEVKNVCIVLSGGNVDLTSLNWV 325
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InterPro; IPR001721; ThrDh_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    enzyme; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C; 2.
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VARIANT 499 49
VARIANT 544 54
SEQUENCE 592 AA; (
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Search completed: June 24, 2003, 06:19:30

21.4713 secs

Job time

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5.1.6
Compugen Ltd.
 GenCore version
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- protein search, using sw model OM protein June 24, 2003, 05:36:57; Search time 19.5287 Seconds Run on:

(without alignments)
722.114 Million cell updates/sec

US-09-889-609B-10

1 MCAQYCISFADVEKAHINIR......SSITWVKQAERPASYQSVSV 340 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		% Ouery			SUMMARIES	, , , , , , , , , , , , , , , , , , ,	
No :	Score	Match	Length	DB	ID	Description	1 1
1			340	7	SRR_HUMAN	homo	sapien
7	1582.5		339	П	SRR_MOUSE	mus m	musculu
m	605		326	Н	YKV8_YEAST	P36007 saccharomyc	romyc
4	265		323	_	YCNE_SCHPO	-	sacch
S	471		329	Н	THD2_SALTY	P11954 salmonella	ella
9	457		329	-	THD2_ECOLI	P05792 escherichia	ichia
7	445	25.6	. 332	Н	Y4TJ_RHISN		ium s
œ	404		513	П	THD1_PASMU	-	rella
6	395.5		513	Н	THD1_HAEIN		hilus
10	390.5		576		THDH_YEAST		romyc
11	376		422	-	THD1_BACSU	P37946 bacillus	ns sn
12	375		. 507	-	THD1_BURCE		lderi
13	369.5		550	П	THDH_ARXAD		aden
14	368		592	П	THD1_ARATH	Q9zss6 arabidopsis	opsis
15	363		595	Н	- 1		rsico
16	362		514	-	THD1_SALTY		ella
17	357		514	П	- 1	_	ichia
18	351.5		416	-	- 1	lacto	occus
19	351		290	-	- 1	cicer	ariet
20	347		415	-	THD1_BACHD.	Q9kc63 bacillus	us ha
21	314.5	18.1	429	Н	- 1	Q10766 mycobacteri	cteri
22	311.5		436	П		Q04513 corynebacte	bacte
23	301.5		427	Н	THD1_MYCLE	-	cteri
24	267.5		362	Η	SDHL_RAT	P09367 rattus norv	norv
25	265.5		328	-	SDHL_HUMAN	2 homo	sapien
56	210		359	~	- 1	~	m tub
27	209.5		311	-	CYSM_BACSU	92	ns sn
28	203		352	Н	THRC_BACSP	33	ns sp.
59	201.5		354	<u>, , , , , , , , , , , , , , , , , , , </u>	THRC_BACHD	Q9k7e3 bacillus	
30	201		307	-1	CYSK_BACSU	~	ns sn
31	200.5	11.6	352	Н	THRC_BACSU	4990	ns sn
. 32	200	11.5	382	, 4	THRC_SYNY3	4193	ocyst
33	198.5	11.4	312	1	CYSK_SYNY3	P73410 synechocyst	ocyst

InterPro; IPR001926; B6_enzyme_beta. InterPro; IPR000634; S/T_dehydrtse. Pfam; PF000291; PALP; 1. PR05TIF: PS00165; DEHYDRATASE_SER_THR; 1. Isomerase; Pyridoxal phosphate.

MIM; 606477

P17324 saccharomyc				P35520 homo sapien							0
SDHL_YEAST	CYSK_MYCTU	CYSK_FLASP	THRC_MYCLE	CBS_HUMAN	CYSK_MYCLE	THRC_MYCTU	CYSM_MYCTU	Y4XP_RHISN	CBS_RAT	THRC_METJA	CYSM_CAMJE
Н	Н	7	_	-	П	٦	T	Н	J	1	П
338	310	307	360	250	310	360	323	336	260	405	299
11.3	11.0	10.9	10.8	10.8	10.6	10.4	10.1	10.0	6.6	9.6	6.6
196.5	191	189	187	187	184.5	181	174.5	173.5	172	171.5	171
34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain;
MEDLINE=20510003; PubMed=11054547;
DeMiranda J., Santoro A., Engelender S., Wolosker H.;
"Human serine racemase: molecular cloning, genomic organization and functional expression.";
Gene 256:183-188(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY
                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF169974; AAG27081.1; .. Oof 27, 2000
EMBL; AK023169; BAB1442.1; ... Gof 27, 2000
Genew; HGNC:14398; SRR.
                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine racemase (EC 5.1.1.-).
                                                                   340 AA
                                                                   PRT;
                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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01-JUN-1994
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P36007;
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                                                                                                     LNAVRSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQA
                                                                                                                                                                                                        KSSIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQT
                                                                                        1 MCAQYCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGA
                                                                                                                                                                                                                                            VVPVGGGGMLAGIATVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGV
                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Strausberg R.;
Submitted (JuL-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the synthesis of D-serine from L-serine.
-!- TISSUE SPECIFICITY: Brain.
-!- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to regulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
   PYRIDOXAL PHOSPHATE (BY SIMILARITY)
                                                                 .
0
                                      340;
                                          Length
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wolosker H., Blackshaw S., Snyder S.H.;
"Serine racemase: a glial enzyme synthesizing D-serine
glutamate-N-methyl-D-asparate neurotransmission.";
Proc. Natl. Acad. Sci. U.S.A. 96:13409-13414(1999)";
               873342C62D5D7B9D CRC64;
                                                                                                                                                                                                                                                                                                                                                          VSPEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV
                                       Score 1735; DB 1
Pred. No. 1e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine racemase (EC 5.1.1.)
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                                                                Mismatches
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              36566 MW;
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100.0%;
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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56
340 AA;
                                       Query Match
Best Local Similarity
Matches 340; Conserv
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                                                                                                                                                                                                                                            1 MCAQYCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 VVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 KSSIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAVLSQHFQT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- COFACTOR: PYRIDOXÁL PHOSPHATE (BY SIMILARITY).
                                                                                                      SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical 34.9 kDa protein in COS9-JEN1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      revealed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tzermia M., Horaitis O., Alexandraki D.;
Tzermia M., Horaitis O., Alexandraki D.;
Trhe complete sequencing of a 24 6 kb segment of yeast chroidentified the known loci URAl, SACI and TRP3, and revealed open reading frames including homologues to the threonine phylorizes, membrane transporters, hydantoinases and the phospholipase A2-activating protein.",
                                                                                                                                                                DB 1; Length
                                                                                                    PYRIDOXAL PHOSPHATE (BY S. B9AE9A9336358728 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSPEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.2%; Score 1582.5; DB 1.89.7%; Pred. No. 4.9e-114; Live 19; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
Pfam: PF00291; PALP: 1.
PROSITE; PS001065; DEHYDRATASE_SER_THR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95028164; PubMed=7941750;
                                                                              Isomerase; Pyridoxal phosphate
BINDING 56 56 PY
                                                                                                                         339 AA; 36359 MW;
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                                                                                                                                                                                Local Similarity 89.7
nes 305; Conservative
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41,
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                                                                                                                                                                                                                                                                                                                    68 VPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVY 127
                                                                                                                                                                                                                                                                                                                                   .28 CEPSDESRENVAKRYTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGG 187
                                                                                                                                                                                                                                                                                                                                                                                                      122 YNRYTEDREQIGRQLAAEHGFALIPPYDHPDVIAGOGTSAKELLEEVGQLDALFVPLGGG 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 NTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                            8 SFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21848401; PubMed=11859360;
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
Gonlies M., Connor R., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
Molls., Pearson D., Quail M.A., Rabbinowitsch E.,
Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
                                                                                                                                                                                                                                                                             Gaps
                                              HSSP; P04968; 1TDJ
SGD; S0001701; YKL218C.
SGD; S0001701; YKL218C.
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR001934; S/T_dehydrtse.
Pfam; PP00291; PALD; I.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
PROSITE; PS00165; DEHYDRATASE_PTRC; 1.
Hypothetical protein; Lyase; PyrIddoxal phosphate.
F3 53 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                      Length 326;
                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                64; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C320.14 in chromosome III.
SPCC320.14 OR SPCC330.15C.
Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                     34.9%; Score 605; DB 1; 41.0%; Pred. No. 3.2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    307 NICIVLSGGNVDLTSSITWVKQAE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              298 KVGIILSGGNVDMKRYATLISGKE 321
2) 228218; CAA82063.1; -; S38061; S38061. P.; S44320. P; P04968: Imm-
 EMBL; X75951; CAA53555.1;
EMBL; Z28218; CAA82063.1;
                                                                                                                                                                                                                  Best_Local Similarity 41.0
Matches 133; Conservative
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PIR; S
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Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
Meltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
Bger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
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Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
Daninguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Cerrutti L., Lowe T., McCombi W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
The genome sequence of Schizosaccharomyces pombe.";
Nature 415:871-880(2002).
Nature 415:871-880(2002).
C. !- COFACTOR: PYRLDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 YDRYKDDREKMAKEISEREGLTIIPPYDHPHVLAGQGTAAKELFEEVGPLDALFVCLGGG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68 VPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVY 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1989 (Rel. 12, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase catabolic (EC 4.2.1.16) (Threonine deaminase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 3.7e-36;
67; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.6%; Score 565; DB 1; 40.3%; Pred. No. 3.7e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL022245; CAA18316.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AL031603; CAA20920.1; -.
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Matches 127; Conservative
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P11954;
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242 RPGNLTYEIVRELVDDIVLVSEDEIRNSMIALIQRNKVITEGAGALACAALLSGKLDSHI 301
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01-NOV-1988 (Rel. 09, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase catabolic (EC 4.2.1.16) (Threonine deaminase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=KIZ ' MG1652,
STRAIN=KIZ ' MG1651,
Pubbed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Griegy J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Gaub B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=K12 / W3110;
MEDLINE-89282418; PubMed=2660107;
Schweizer H., Datta P., "The complete nucleotide sequence of the tdc region of Escherichia
                                                                  SIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN-0157.H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Rose D.J., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=K12 / W3110;
MEDLINE=87092415; PubMed=3540965;
Datta P., Goss T.J., Omnaas J.R., Patil R.V.;
"Covalent structure of biodegradative threonine dehydratase of Escherichia coli: homology with other dehydratases.";
Proc. Natl. Acad. Sci. U.S.A. 84:393-397(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                  QHFQTVSPEVKNICIVLSGGNVDLT--SSITWVKQA 329
                                                                                                                                                                                        302 ONRKTVS-----IISGGNIDLSRVSOLTGLVDA 329
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MEDLINE=21156231; PubMed=11258796;
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                                                                                                                                                                                                                                                                                                                                                                                 09, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                  STANDARD;
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P05792;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-S 242
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                                                                                                                                SEQUENCE FROM N.A.

STRAIN-IT2 / SGSC1412 / ATCC 700720;

MEDLINE-21534948; pubMed=11677609;

MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Muyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Kyan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENZYME REGULATION: EACH PROTEIN MOLECULE CAN BIND UP TO FOUR MOLECULES OF AMP, WHICH ACTS AS AN ALLOSTERIC ACTIVATOR TO THE ENZYME. THE ENZYME IS ALSO INHIBITED BY ALPHA-KETO ACIDS AND OTHER CATABOLITES. IT IS ALLOSTERICALLY INHIBITED BY ISOLEUCINE AND ALLOSTERICALLY ACTIVATED BY VALINE.

PATHWAY: Threonine catabolism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kim S.S., Datta P.;
"Chemical characterization of biodegradative threonine dehydratases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROUZY1; raur, 1.
2; PS00165; DEHYDRATASE_SER_THR; 1.
Pyridoxal phosphate; Allosteric enzyme; Complete proteome.
58 58 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 329;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K -> I (IN REF. 2).
C1C619B021DE817C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64; Mismatches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.1%; Score 471; DB 1; 36.6%; Pred. No. 5.9e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro, IPR001926, B6_enzyme_beta.
InterPro, IPR000634, S/T_dehydrtse.
Pfam; PF00291; PALP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-24.
MEDLINE-83023208; PubMed=6751404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE008849; AAL22117.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from two enteric bacteria.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HOMOTETRAMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                         Nature 413:852-856(2001).
                   Salmonella typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; B22317; B22317.
StyGene; SG10390; tdcB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity
Matches 123; Conserv
                                                                                      NCBI_TaxID-602;
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P04968;
                                                                                                  Y4TJ_RHISN
P55664;
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Matches
                                                                                      Y4TJ_RHISN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     295
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                                                                                                                                                                                                      OTHER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 VGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              243 SIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                      -!- CATALYTIC ACTIVITY: L-threonine + H(2)0 = 2-oxobutanoate + NH(3)
                                                                                                                                                                                                                                                                  -i- INDUCTION: TRANSCRIBED IN RICH MEDIUM. IT IS MADE ANAEROBICALLY.
                                                          Kim S.S., Datta P.; "Chemical characterization of biodegradative threonine dehydratases from two enteric bacteria.";
                                                                                                                                                                       ENZYME REGULATION: EACH PROFEIN MOLECULE CAN BIND UP TO FOUR MOLECULES OF AMP, WHICH ACTS AS AN ALLOSTERIC ACTIVATOR TO THE ENZYME. THE ENZYME IS ALSO INHIBITED BY ALPHA-KETO ACIDS AND OT CATABOLITES. IT IS ALLOSTERICALLY INHIBITED BY ISOLEUCINE AND ALLOSTERICALLY ACTIVATED BY VALINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
and genomic comparison with a laboratory strain K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 AA; 35232 MW; E7DF018FCCF743B1 CRC64;
                                                                                                               AND
                                                                                             Biochim. Biophys. Acta 706:27-35(1982).
-!- FUNCTION: ACTS ON BOTH SERINE AND THREONINE,
CONSIDERED AS A HYDROXY AMINO ACID DEAMINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyridoxal phosphate; Allosteric enzyme; Cc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.3%; Score 457; DB 1; 36.6%; Pred. No. 6.9e-28; ive 65; Mismatches 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
                                                                                                                                                                                                                                         PATHWAY: Threonine catabolism. SUBUNIT: HOMOTETRAMER.
                                                                                                                                                               -! - COFACTOR: PYRIDOXAL PHOSPHATE.
                                   SEQUENCE OF 1-25.
MEDLINE=83023208; Pubmed=6751404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000393; AAC76152.1; -. EMBL; AE005540; AAG58248.1; -. EMBL; AP002564; BAB37420.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; M21312; AAA24660.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M23638; AAA24661.1; -. EMBL; U18997; AAA57921.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                        X14430; CAA32593.1; -
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Best Local Similarity 36.69
Matches 121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EcoGene; EG10990; tdcB
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HSSP; P04968; 1TDJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative threonine dehydratase (EC 4.2.1.16) (Threonine deaminase).
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-!- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
BUT LACK THE C-TERMINAL DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97305956; PubMed-9163424;
Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae
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1ive 70; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PYRIDOXAL PHOSPHATE.
A46DE121CC33519F CRC64;
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InterPro; IPR000634; S/T_dehydrtse.
Pfam; PF00291; PALP; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Pypothetical protein; Isoleucine biosynthesis; Lyase;
Pyridoxal phosphate; Plasmid.
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      324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 AA
296 QHFQTVSPEVKNICIVLSGGNVDLT--SSIT
                                                                                   302 QNRKTVS------IISGGNIDLSRVSQIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhizobium sp. (strain NGR234).
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nes 109; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rhizobiaceae; Rhizobium.
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HSSP; P04968; 1T
TIGR; HI0738.1;
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                |: |:|||| | : :|| |: ||||:|| | | :: :| :: : : : VIAASAGNHAQGVALSAKHLGLRALIVMPQNTPSIKVDAVRGFGGEVLLHGANFDEAKAK 140
DGVKSSIGL-NTW--PIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVL 294
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                                                                                                                                                                                                                                                                                                                                                         May B.J., Zhang Q., Li L.L. Paustian M.L., Whittam T.S., Kapur V.; "Complete genomic sequence of Pasteurella multocida Pm70."; Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).

-!- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from threonine in a two-step reaction. The first step is a dehydration of threonine, followed by rehydration and liberation of ammonia.
-!- CATALYTIC ACTIVITY: L-threonine + H(2)0 = 2-oxobutanoate + NH(3) +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- PATHWAY: Isoleucine biosynthesis; first step.
-!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pasteurella
                                                                                                                                                                      15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine debydatase blosynthetic (EC 4.2.1.16) (Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 513;
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Pfam; PF00291; Thr_dehydrat_C; 2.
TIGRFAMs; TIGRFAMs; 1.
PROSITE: PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
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                                                                                                                                               513 AA.
                                                                   | | : : : | | | : | S---GKVAARGGSVGVVLSGONIDM 315
                                                  SQHFQTVSPEVKNICIVLSGGNVDL 319
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InterPro; IPR000634; S/T_dehydrtse.
InterPro; IPR001721; ThrDh_C.
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                              MEDLINE=21145866; PubMed=11248100;
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Matches 98; Conservative
                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                      Pasteurella multocida.
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                                                                                                                                                                                                                                        ILVA OR PM1624.
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238
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
AKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMLAGIAITVK 198
                                                                                                                                                                                                                                                                                                                                                                               258 DIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVKNICIVLSGGNV 317
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                                              201 QLMPEIKVIGVESKDSACLYRALKAGKPI-DLDRVGLFADGVAVKRIGDETFRVCQQYID
                                                                                                                                                             ALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SSIGLNTWPIIRDLVD
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Submitted (SEP-1995) to the SWISS-PROT data bank.
-!- FUNCTION: Catalyzes the formation of alpha-Ketobutyrate from
threonine in a two-step reaction. The first step is a dehydration
of threonine, followed by rehydration and liberation of ammonia.
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MEDLINE=95350630; PubMed=7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
Felischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M.,
McKenlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedlom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- CATALYTIC ACTIVITY: L-threonine + H(2)0 = 2-oxobutanoate + NH(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- PATHWAY: Isoleucine biosynthesis; first step.
-i- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
-i- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase biosynthetic (EC 4.2.1.16)
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Haemophilus influenzae.
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EDENTIFICATION
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CATALYTIC ACTIVITY: L-threonine + H(2)0
                                                                                                                                                                                                                                                                                                                                                                                                                          Transit peptide; Allosteric enzyme.
TRANSIT 1
                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C; 2.
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ID THD1_BACSU STANDARD;
AC P37946;
D1 01-0CT-1994 (Rel. 30, Created)
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EMBL; U18839; AAB64641.1; -.
PIR; A01150; DWBYT.
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365 VPILSGANMN 374
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259
576 AA;
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SGD; S0000888; ILV1
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                                                                                                                                                                                                                                                                                                                                                                                                                                   251 IIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVKNICI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                  71
                                                                                                                                                                                                                                 12 VEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDA
                                                                                                                                                                                                                                                                   72 LERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPS
                                                                                                                                                                                                                                                                                                                         DESRENVAKRVTEETEGIMVHPNQEPAVIAGOGTIALEVLNQVPLVDALVVPVGGGGMLA
                                                                                                                                                                                                                                                                                                                                                                                              21; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-S288C / ABB92;
Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R., Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M. Chung E., Duncan M., Guzman E., Hartzell G., Hunicke-Smith S., Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D., Hyman R., Kayser A., Namath A., Norgren R., Oefner P., Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V., Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
Submitted (DEC-1994) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nilsson-Tillgren T.: "Nucleotide sequence of the gene for threonine deaminase (ILV1) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                            Length 513;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.2.1.16)
                                                                                                                                                                                       Indels
                                                                                                                                 DF42CA8B6FDE4CD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----TSSITWVKQAERPASY 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 ILSGANLNFHTLRYVSERCEIGENREALLAVTMPEQPGSF 353
                                 Pfam: PF00291; PALP; 1. Pfam: PF00291; PALP; 1. Pfam: PF00585; Thr_dehydrat_C; 2. Pfam: PF00585; Thr_dehydrat_C; 2. PR051TE, P500165; DEHYDRATASE_SER_THR; 1. Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase, mitochondrial precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Kielland-Brandt M.C., Holmberg S., Petersen J.G.L.,
                                                                                                                                                         Query Match 22.8%; Score 395.5; DB 1; Best Local Similarity 29.7%; Pred. No. 6.3e-23; Matches 101; Conservative 71; Mismatches 147;
                                                                                                                     PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    576 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carlsberg Res. Commun. 49:567-575(1984).
InterPro; IPR001926; B6_enzyme_beta.
            InterPro; IPR000634; S/T_dehydrtse.
InterPro; IPR001721; ThrDh_C.
                                                                                                                                 56662 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLSGGNVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Threonine deaminase)
                                                                                                                                 513 AA;
                                                                                                        Complete proteome.
BINDING 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILV1 OR YER086W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THDH_YEAST
                                                                                                                                SEQUENCE
                         InterPro;
                                                                                                                                                                                                                                          19
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 SYYDVINESPISQGVGLSSRLNTNVILKREDLLPVFSFKLRGAYNMIAKL--DDSQRN-Q 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78 AVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV-YCEPSDESRE 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  137 NVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPL---VDALVVPVGGGGMLAGI 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 GAYLKRVAPHIKIIGVETYDAATLHNSLORNORTP-LPVVGTFADGTSVRMIGEETFRVA 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEV---KNIC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 QQVVDEVVLVNTDEICAAVKDIFEDTRSIVEPSGALSVAG-MKKYISTVHPEIDHTKNTY 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 NIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    = 2-oxobutanoate + NH(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphate;
                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: Mitochondrial. SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                    INHIBITS WHILE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15;
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PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Mitochondrion; Pyridoxal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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THREONINE DEHYDRATASE.
PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I -> T (IN REF. 1).
0801BCBD7EEDDC1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60; Mismatches 130;
                                                                                                                                                                     PATHWAY: Isoleucine biosynthesis; first step. SUBUNIT: HOMOTETRAMER.
                                                                                                    ALLOSTERICALLY
                                                                                                                                 THIS ENZYME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.5%; Score 390.5; DB 1 33.9%; Pred. No. 1.8e-22;
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                                                                                                 ENZYME REGULATION: ISOLEUCINE AL VALINE ALLOSTERICALLY ACTIVATES
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InterPro; IPR000634; S/T_dehydrtse.
InterPro; IPR001721; ThrDh_C.
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us-09-889-609b-10.rsp

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-!- COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                    15
139
422 AA;
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                                                                                                                                                                                                                                                   Complete proteome.
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P53607;
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                                                                                                                                                                                                                                                                                        CONFLICT
                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Runst F. Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
Agevedo V. Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
R. Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
R. Brouillet S., Bridgion J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
R. Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
R. Denizot F., Devine K.M., Dusterhoft A., Erlich S.D., Emmerson P.T.,
R. Eritz C., Fulita M., Fulita Y., Fuma S., Galiszia A., Galleron N.,
A Ghims S.Y., Glaser P., Goffeau A., Gollghtly E.J., Grandl G.,
R. A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Lorins B., Karamata D., Kasahara Y., Klaenr Blanchard M., Klein C.,
R. Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
A Lee S.M., Levine A., Liu H., Masuda S., Maulel C., Medique C.,
R. Median N., Mellado R.P., Mizuno M., Mosstl D., Nakai S., Noback M.,
R. Moone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
R. Perscan E., Pulic P., Purnelle B., Rapport G., Rey M., Reynolds S.,
R. Asado T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Schleich S., Takabashi H., Takemaru K.,
R. Sakiguchi J., Sekwaka A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Scockin A., Tacconi E., Takagi T., Takabashi H., Takemaru K.,
R. Schiguchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Varia A., Wanbutt R., Wedler E., Wedler H., Wanner K., Yasamoto H., Yanamoto H., Yanamoto H., Yanamoto H., Yasamoto H., Yasanote S., Wochida K., Yoshikawa H.F., Zoshikawa H.F., Coshikawa H.F., Zoshikawa H.F., Coshikawa H.F., Coshikawa H.F., Caphilus S., R., Phillis F., Phillis
                                                                                                                                                                                                                                                                                                                                                          "Sequence analysis of the Bacillus subtilis chromosome region between
the serA and kdg loci cloned in a yeast artificial chromosome.";
Microbiology 142:2005-2016(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -i-FUNCTION: Catalyzes the formation of alpha-ketobutyrate from threonine in a two-step reaction. The first step is a dehydration of threonine, followed by rehydration and liberation of ammoniation of ammoniation and Liberation of Liberation of Liberation of Liberation of Liberation of Experiments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PATHWAY: Isoleucine biosynthesis; first step. SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                     Sorokin A.V., Azevedo V., Zumstein E., Galleron N., Ehrlich S.D.,
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase biosynthetic (EC 4.2.1.16) (Threonine
                                                                                                                                                                                                          Armpriester J.M. Jr., Fink P.S.;
Submitted (XXX-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                              Bacillales; Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COFACTOR: PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                  STRAIN=168 / Marburg;
MEDLINE=96349105; PubMed=8760912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 390:249-256(1997).
                                                                                                              Bacteria; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                           Bacillus subtilis.
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                NCBI_TaxID=1423;
                                                          deaminase).
                                                                                                                                                                                        STRAIN=168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 YCEPSDESRENVAKRVTE--ETEG-IMVHPNQEPAVIAGQGTIALEVLNQVPL-VDALVV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 SVGGGGLLSGVGTYLKNVSPDTKVIAVEPAGAASYFESNKAGHVV-TLDKIDKFVDGAAV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 PVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK- 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 SSIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTV 301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 IQVKHILKAHQNVKDVVIHTPLQRNDRLSERYECNIYLKREDLQVVRSFKLRGAYHKMKQ 70
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Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
-:- FUNCTION: Catalyzes the formation of alpha *ketobutyrate from
threonine in a two-step reaction. The first step is a dehydration
of threonine, followed by rehydration and liberation of ammonia.
-:- CATALYTIC ACTIVITY: L-threonine + H(2)0 = 2-oxobutanoate + NH(3) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                              PYRIDOXAL PHOSPHATE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Burkholderia cepacia (Pseudomonas cepacia).
Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase blosynthetic (EC 4.2.1.16) (Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 1.5e-21;
64; Mismatches 143; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46701 MW; 3027A5ED87084140 CRC64;
                                                                                                                                                                                                                           Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                            H -> D (IN REF.
V -> A (IN REF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.7%; Score 376;
                                                                                                         Subtilist; BG10673; ilva.
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR001634; S/T_dehydrtse.
InterPro; IPR001721; ThrDh_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --KGKNVVCVVSGGNNDI 321
EMBL, M58606, AAA22549.1; -. EMBL, L77246, AAA96639.1; -. EMBL, Z99115; CAB14095.1; -. HSSP; P04968; ITDJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 31.1 Matches 99; Conservative
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THD1_ARATH
       NAME OF THE PROPERTY OF THE PR
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                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMIS outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 IGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSP 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 PSDESRENV---AKRVTEETEGIMVHPNQEPAVIAGQGTIALEVL--NQVPLVDALVVPV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OAGESYSDAYAHALKVQEERGLTFVHPFDDPYVIAGQCTIAMEILRQHQGP-IHAIFVPI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 HLTPVLTSSILNQL-----TGRNL-----FFKCELFOKTGSFKIRGALNAVRSLVP 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| :||: | :||| | : : ||| | : : ||| | : : ||| | : : ||| | : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : ||| | : : : || | : : : ||| | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | : : : || | :
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                                 SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Dipodascaceae; mitosporic Dipodascaceae; Arxula.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase, mitochondrial precursor (EC 4.2.1.16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.6%; Score 375; DB 1; Length 50' 33.3%; Pred. No. 2.3e-21; indels ive 59; Mismatches 125; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E9A5D110B0597664 CRC64;
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PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Pyridoxal phosphate.
BINDING 52 PYRIDOXAL PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98398049; PubMed=9730281;
Wartmann T., Roesel H., Kunze I., Bode R., Kunze G.;
PATHWAY: Isoleucine biosynthesis; first step. SUBUNT: HOMOTETRAMER (BY SIMILARITY)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
InterPro; IPR001721; ThrDh_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55326 MW;
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ENQTLVAVTSGANMN 314
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Best Local Similarity 33.33
Matches 105; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEV----KNICIV 311
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                                     transformation marker.";
Yeast 14:1017-1025(1998)
-!- CATALYTIC ACTIVITY: L-threonine + H(2)0 = 2-oxobutanoate + NH(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS; TIGRO1124; ilva_2Cterm; 1.
PROSITE; PSO0165; DEHYDRATASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Mitochondrion; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
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92SS6: 09SPP1;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase biosynthetic, chloroplast precursor (EC 4-2.1.16) (Threonine deaminase) (TD).
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Arxula adeninivorans LS3
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                                                                                                                                                                                                                                                                                                          first step.

    -!- PATHWAY: Isoleucine biosynthesis; first
    -!- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
    -!- SUBCELLULAR LOCATION: Mitochondrial.

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                                                                                                                                                                                                                                                   -! - COFACTOR: PYRIDOXAL PHOSPHATE
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Salanoubat M., Lemcke K., Rieger M., Perez-Alonso M., Obermaier B.,
Ratmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
Delseny M., Boutry M., Grivell L.A., Mache R., Puigdomench P.,
RA De Simone V., Choisne N., Ariguenave F., Robert C., Brottler P.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Baradt P., Nyakatura G.,
Ra Conrad A., Hornischer K., Kauer G., Lochhert T.-H., Nordsiek G.,
Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Ravarro P., Collado C., Perez-Perez A., Ottenwaelder B., Masuy D.,
RA Gooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
R. Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
R. Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
R. Rossy T.H., Haas B., Schoof H., Makashum K., Kishida Y.,
R. Fraser C.M., Kanko T., Nakamura Y., Sato S., Kato T., Asamizu E.,
R. Sasamoto S., Kimura T., Idesawa K., Kawashuma K., Kishida Y.,
R. Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Muraki A.,
R. Sequence and analysis of chromosome 3 of the plant Arabidopsis
R. Haliana., R. A., Vanada M., Tabata S.;
R. Haliana., R., Rabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 408:820-822(2000).
--- FUNCTION: Catalyzes the formation of alpha-ketobutyrate from threonine in a two-step reaction. The first step is a dehydration of threonine, followed by rehydration and liberation of ammonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
ENZYME REGULATION: Allosterically inhibited by isoleucine. Strain.
GM11b is isoleucine feedback insensitive and is resistant to the
                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: L-threonine + H(2)0 - 2-oxobutanoate + NH(3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mourad G., Emerick R., Smith A.; "Molecular cloning an isoleucine feedback insensitive threonine dehydratase/deaminase of Arabidopsis fhaliana line GM11b.";
                                                                                                                                                                                                     STRAIN=cv. Columbia;
Mourad G., Emerick R., Marion A., Smith A.;
"Cloning and sequencing of a cDNA encoding threonine dehydratase/deaninase of Arabidopsis thaliana.";
(In) Plant Gene Register PGR98-199.
                                                                                                                                                                                                                                                                                                                                                                                                                  genomic clone, including
                                                                                                                                                                                                                                                                                                                                                                                  Moirad G.S., Smith A.M.; "Molecular characterization of the genomic clone, including promoter sequences, of threonine dehydratase/deaminase from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: Isoleucine biosynthesis; first step. SUBCELLULAR LOCATION: Chloroplast (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antimetabolite L-O-methylthreonine.
PATHWAY: Isoleucine biosynthesis; first step
                             (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. GM11b;
MEDLINE=20144028; PubMed=10677454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
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AT3G10050 OR T22K18.12
                        Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 TEGI-MVHPNQEPAVIAGQGTIALEVLNQV--PLVDALVVPVGGGGMLAGIAITVKALKP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETI------ADGVK-SSIGLNTWPIIR 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 SPLQLAKKLSKRLGVRMYLKREDLQPVFSFKLRGAYNMMVKLPADQL---AKGVICSSAG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     337 NLMDGVVLVTRDAICASIKDMFEEKRNILEPAGALALAGA-EAYCKYYGLKDVNVVAITS 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 TPVLTSSILNOLTGRNLFFKCELFOKTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSG 85
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SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRPAMS; TIGRO1124; ILVA_2Cterm; 1.
PROSITE; PSO0165; DEHYDRATASE_SER_THR; 1.
Stoleucine biosynthesis; Lyase; Chloroplast; Pyridoxal phosphate; Allosteric enzyme; Transit peptide.
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THREONINE DEHYDRATASE BIOSYNTHETIC.
PYRIDOXAL PHOSPHARE (BY SIMILARITY).
R -> C (IN STRAIN GM11B).
R -> H (IN STRAIN GM11B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
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15-JUN-2002 (Rel. 41, Last annotation update)
Threonine dehydratase biosynthetic, chloroplast precursor
(EC 4-21.16) (Threonine deaminase) (TD)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.2%; Score 368; DB 1; Length 59
30.2%; Pred. No. 9.6e-21;
Live 65; Mismatches 129; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR001634; S/T_dehydrtse.
InterPro; IPR001721; ThrDh_C.
Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum (Tomato)
                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF221984; AAF32370.1; EMBL; AF177212; AAD54324.1; EMBL; AC010927; AAF04418.1; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           592
141
499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P04968; 1TDJ
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Job time : 20.5287 secs

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                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113 SPLELAEKLSDRIGVNFYIKREDKQRVFSFKLRGAYNMMSNLSREELD---KGVITASAG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV-YCEPSDESRENVAKRVTE 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 VKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SSIGLNTWPIIRDLVDDIFTV 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26 TPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 TEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQ-HFQTVSPEVKNICIVLSGGNVDLT 320
                                                                                                                                             structure, and upregulation in floral organs.";
Proc. Natl. Acad. Sci. U.S.A. 88:2678-2682(1991).
-!- CATALYTIC ACTIVITY: L-threonine + H(2)0 = 2-oxobutanoate + NH(3) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145 ETEGI-MVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMLAGIAITVKALKPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12; Gaps
                                                                                                                                                                                                                                                                                                                                        500-FOLD. SIMILARITY: BELONGS TO THE SERINE/THREONINE DEHYDRATASE FAMILY.
                                                                                                                                                                                                                                                                                                                       -!- MISCELLANEOUS: EXPRESSION IN MATURE FLOWERS IS INCREASED OVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGRO1124; ilva_20term; 1.
NOSSITE; PSO0165; DEHVDRAFASE_SER_THR; 1.
Isoleucine biosynthesis; Lyase; Chloroplast; Pyridoxal phosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THREONINE DEHYDRATASE BIOSYNTHETIC.
PYRIDOXAL PHOSPHATE (BY SIMILARITY);
AC430BB5DD9F0348 CRC64;
                                                                                                                н
Н
                                                                                                                                                                                                                      -!- COFACTOR: PYRIDOXAL PHOSPHATE.
-!- ENZYME REGULATION: ALLOSTERICALLY INHIBITED BY ISOLEUCINE.
-!- PATHWAY: ISOLeucine biosynthesis; first step.
-!- SUBBUNIT: HOMOTERRAMER.
-!- SUBCELLULAR LOCATION: Chloroplast.
                                                                                                              Samach A., Hareven D., Gutfinger T., Ken-Dror S., Lifschitz "Blosynthetic threonine deaminase gene of tomato: isolation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 20.9%; Score 363; DB 1; Length 595; Best Local Similarity 32.1%; Pred. No. 2.3e-20; Matches 96; Conservative 62; Mismatches 129; Indels
 Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                       AND SEQUENCE OF 52-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P04968; 1TDJ.
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
InterPro; IPR001721; ThrDh_C.
Pfam; PF00291; PALP; 1.
Pfam; PF00585; Thr_dehydrat_C; 2.
                                                     SEQUENCE FROM N.A., AND SEQUENCE (STRAIN-CV. TINY TIM LA154;
MEDLINE-91187855; Pubmed-2011578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64937 MW;
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Search completed: June 24, 2003, 06:19:31

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GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on:

June 24, 2003, 02:01:55; Search time 57 Seconds
(without alignments)
5477.139 Million cell updates/sec

Title:
US-09-889-609B-1

Perfect score:
1 atgtgtgctcagtactgcat......ttaccagacggtctgtttaa 1018
Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched:
441362 seqs, 153338381 residues
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IES	Description	-300A-3 Sequence 3, Appli	-1 Sequence 1.	-1 Sequence 1,	1 Sequence 1,	-5 Sequence 5,	-7 Sequence 7,	Sequence 8,	388-1 Sequence 1,	Sequence 5,	Sequence 7,	388-8 Sequence 8,	-1	-877-5 Sequence 5, Appli	877-7 Sequence 7,	877-8 Sequence 8,	205-1 Sequence 1,	205-5 Sequence 5,	Sequence 7,	Sequence 8,	1 Sequence 1,	Sequence 5,	7 Sequence 7,	. Sequence 8,	1 Sequence 11	4 Sequence 14,	Sequence 2,	
SUMMARIES	ID	US-09-789-300A	US-09-789-300A	US-09-153-599A	US-08-628-039	US-08-628-039	US-08-628-039	US-08-628-039-8	US-08-673-388-1	us-08-673-	US-08-673-388-7	US-08-673-	US-08-614-	US-08-614-	US-08-614-	US-08-614-	US-08-912-	US-08-912-	US-08-912-205-7	US-08-912-205-8	-004-04-60-SD	US-09-440-400-5	US-09-440-400-	US-09-440-400-8	US-08-403-866-1	US-08-232-463-1	US-09-088-435-2	
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	Score	807.8	807.8	62.2	9.09	9.09	9.09	9.09	9.09		9.09		9.09	9.09	9.09	9.09	9.09	9.09	9.09	9.09	9.09	9.09	9.09	9.09	52.8	46.6	38.8	
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Sequence 6, Appli . Sequence 75, Appl Sequence 10, Appli Sequence 1, Appli Sequence 25, Appli Sequence 29, Appli Sequence 59, Appli Sequence 50, Appli S	
US-08-878-474-6 US-09-227-357-75 US-08-238-165A-207 US-08-238-165A-207 US-09-449-285A-1 US-09-449-285A-1 US-09-449-285A-1 US-09-449-285A-1 US-08-103-739B-1 US-08-103-739B-1 US-08-118-1 US-09-211-416-1 US-09-211-416-1 US-09-211-416-1 US-09-211-416-1 US-09-211-416-1 US-09-113-854-39 US-09-113-854-39 US-09-113-854-59 US-09-118-627-59	
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33 34 33 38 33 38 33 38 31 1 1 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	
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ALIGNMENTS

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Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000

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Minimum DB Maximum DB Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued_Patents_NA:*

Database :

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GACTCTATCCACCTCACCCCAGTGCTAACAAGCTCCATTTTGAATCAAATAGCAGGGCGC 120
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GENERAL INFORMATION:

APPLICANT: Meyers, Rachel

APPLICANT: Rudolph-Towen, Laura A.

APPLICANT: Rudolph-Towen, Laura A.

TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate

TITLE OF INVENTION: Dependent Enzyme Family Member and Uses Therefore

FILE REFERENCE: 35800/208926

CURRENT APPLICATION NUMBER: US/09/789, 300A

CURRENT FILING DATE: 2001-02-20

PRIOR APPLICATION NUMBER: US 60/183, 208

PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                   Length 1020;
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                                                                                                                                                                                                                                                                                                                Score 807.8; DB 4;
Pred. No. 6.8e-267;
0; Mismatches 122;
                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
             Sequence 3, Application US/09789300A Patent No. 6458576
                                                                                                                                                                                                                                                                                                                79.48;
87.78;
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Best Local Similarity 87.7
Matches 894; Conservative
                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                        1020
US-09-789-300A-3
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OY 1 ATGTGGCTCAGTACTGCATCTTGCTGATGTTGAAAAGGTCATATCAACATTCAA 60	189 AATCTTTCTTCAAATGTGAACTCTTCCAGAAACAGGATCTTTTAAGATTCGTGGTGCT 2 181 CTTAATGCCATCAGAGGCTTAATTCCTGACACGCCGGAAGAGAAGCCCAAAGCCCTAGTT 2 181 CTTAATGCCATCAGAGGCTTAATTCCTGACGCCGAAGAGAAGCCCAAAGCCGTGTT 2 249 CTCAATGCCGTCAGAAGCTTGGTTCCTGATGCTTTAGAAAGGAAGCCGAAAGCTGTTGTT 3 241 ACTCACAGCGGAAACCATGGCCAAGCTCTCACCTATGCTGCTAAACTGGAAGGAA	Db 309 ACTCACAGCAGGGAAACCATGGCCAGGCTCTCACCTATGCTGCCAAATTGGAAGGAA	Oy 421 AGAATTATGCAAGAAGCCATCTTGGTCCATCCCAGGAGCCTGCAGTGATA 480	541 GTGGTACCAGTAGGAGGAGGAGGAATGGTTGCTGGAATAGCATTACAATTAAGGCCCTG	0y 661 AAACTGAAAGGAGAACTGACCCCAATCTTCATCCTCCAGAAACCATAGCAGATGGTGTC 720 1 1111 1 111 1111 111 111	CAGCATTTCCAAACA	Oy 959 -CCTCCCTGAACTGGGTGGGCTGAACGGCCAGCTCCTTACCAGACGGTCTGTTT 1016
Qy 361 TATGGACCATCGATAGTATACTGTGACCCAAGTGACGAGTCCAGAGAAAAGGTCACTCAA 420 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		661 AAACTGAAAGGAAACTGACCCCCAATCTTCATCCTCCAGAAACCATAGGAGATGGTGTC 72	781 ACTGTCACGAAGATGAATCAAGTATGCAACCCAGCTGTGGGGGGAGAATGAAACTG 84 1111111 1 111111 1 1111111 1	OY 901 GTCTCTCCAGAAGTAAAGAACGTCTGCATTGTACTCAGTGGGGGGAATGTAGACCTAA 958 DD 11 11 11 11 11 11 11 11	RESULT 2 US-09-789-300A-1 Sequence 1, Application US/09789300A Sequence 1, Application US/09789300A Sequence 1, Application US/09789300A GENERAL INFORMATION: APPLICANT: Meyers, Rachel TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate TITLE OF INVENTION: Dependent Enzyme Family Member and Uses Therefore FILE REFERENCE: 35800/208926 CURRENT APPLICATION NUMBER: US/09/789,300A	CURRENT FILING DATE: 2001-02-20 PRIOR APPLICATION NUMBER: US 60/183,208 PRIOR FILING DATE: 2000-02-17 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0 LENGTH: 1770 TYPE: DNA TYPE: DNA PRIOR FILING Sapiens	sapi (1

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Hinchee, Maud A. W.
Clemente, Thomas E.
Connor-Ward, Dannette V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                  Sequence 1, Application US/08628039 Patent No. 5942660
                                                                                                                                              Padgette, Stephen R.
Stark, David M.
                                                                                         Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bond, Gary
REGISTRATION NUMBER: 29,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3412
                                                                         Gruys, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                     Fedele, Mary J.
Fry, Joyce E.
Howe, Arlene R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 13-MAR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                              Rozman, Renee J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1545 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (314)695-5435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        double
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                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                      St. Louis:
: Missouri
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Best Local Similarity
                                                     GENERAL INFORMATION:
APPLICANT: Gruys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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APPLICANT:
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APPLICANT:
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US-08-628-039-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1996 GCGCGCTGCTGCTGCAACGGCCGAAGCTGGTCGAACCCGCCGCGCGTCGCGG 1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2236 TCAGCGGCATCGCCGCGGCGGTGAAGGCGGAGCACCCGCAGGTGCGGGTGCTCGCCGTCC 2177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    509 TGCTGAACCAGGTTCCCTTGGTAGATGCACTGGTGGTACCAGTAGGAGGAGGAGGAATGG 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               746 GGCCTATTATAAGAGACCTTGTGGATGATGTCTTCACTGTCACCGAAGATGAAATCAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        689 ITCAICCICCAGAAACCAIAGCAGAIGGIGICAAAICCAGCAIIG---GCIIGAAIACCI
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                                                      Method for Strain Improvement of Erythromycin Producing Bacterium 13
                                                                                                                                        ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza
                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 62.2; DB 4; Pred. No. 9.3e-11; 0; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FER2159P0041US
                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/153,599/
                                                                                                                                                                                                                                                                                                         PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mueller, Lisa V.

REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: FER21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-153-599A-1
             GENERAL INFORMATION:
APPLICANT: Weber, J. Mark
APPLICANT: Luu, B. Minh
TITLE OF INVENTION: Method
TITLE OF INVENTION: Erthrol
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
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48.98;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2299 base pairs
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Best Local Similarity 48.9%
Matches 197; Conservative
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STRANDEDNESS: single
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                                                                                                                                                                                                 Illinois
                                                                                                                                                                                                                  U.S.A.
                                                                                                                                                                          Chicago
                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                               ZIP: 60601
                                                                                                                                                                                                                COUNTRY:
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INVENTION: Methods of Optimizing Substrate Pools and INVENTION: Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval INVENTION: in Bacteria and Plants
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                                                                                                                                                                             3: Gary M. Bond, Monsanto Company, A3SB 800 No. 5942660th Lindbergh Boulevard
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APPLICATION NUMBER: US/08/628,039
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Pred. No. 2.5e-10;
0; Mismatches 224;
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Methods of Optimizing Substrate Pools and
Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval
in Bacteria and Plants
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                                                                                          280 GTCGCGTTTTCTTCTGCCGCGTTAGCCGTGAAGGCCCTGATCGTTATGCCAACCGCCACC 339
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                                                                      211 ACGCCAGAAGAGAAGCCCAAAAGCCGTAGTTACTCACAGCAGCGGAAACCATGGCCAAGCT
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     Length 1545;
                                     Indels
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 Score 60.6; DB 2;
Pred. No. 2.5e-10;
); Mismatches 224;
                                    0; Mismatches
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Connor-Ward, Dannette
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Stark, David M.
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Kishore, Ganesh M.
Slater, Steven C.
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   6.0%;
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Query Match
Best Local Similarity 46.5
Matches 195; Conservative
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MEDIUM TYPE: Floppy
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TITLE OF INVENTION:
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CLASSIFICATION:
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Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalera
in Bacteria and Plants
   510
                                                                                                                                           GTGCCGCCGTTCGACCATCCGATGGTGATTGCCGGGCAAGGCACGCTGGCGCTGGAACTG 519
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                                                                                                                                                                                                                 GTCCATCCCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGAACAATTGCCCTGGAAGTG
                                                                                                                       CTGAACCAGGTTCCCTTGGTAGATGCACTGGTGGTACCAGTAGGAGGAGGAGGAATGGTT
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PatentIn Release #1.0, Version #1.30
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STREET: 800 No. 5942660th Lindbergh Boulevard
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                                                                                                                                                                                                                                                                                                                 Sequence 5, Application US/08628039
                                                                                                                                                                                                                                                                                                                                                                                                                    Slater, Steven C.
Padgette, Stephen R.
Stark, David M.
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REGISTRATION NUMBER: 29,283
                                                                                                                                                                                                                                                                                                                                                                                  Mitsky, Timothy A. Kishore, Ganesh M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3412
                                                                                                                                                                                                                                                                                                                                                                   Gruys, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemente, Thomas
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 13 *MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fry, Joyce E.
Howe, Arlene R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rozman, Renee J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1545 base pairs
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APPLICATION NUMBER: US
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EDNESS: double
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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Missouri
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                                                                                                                                                                                                                                                                                                                                 Patent No. 594266(
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US-08-628-039-5
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271 CTCACCTATGCTGCTAAACTGGAAGGAATTCCTGCTTACATTGTGGTTCCCCAAACAGGT 330
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                                                                                                                                                                                                                         Version #1.30
    M. Bond, Monsanto Company, A3.
5942660th Lindbergh Boulevard
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Pred. No. 2.5e-10;
0; Mismatches 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                             29,283
ER: 38-21(13585)A
                                                                                                                                                                                                     SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0,
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/628,039
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APPLICANT: Gruys, Kenneth J.
                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 29,283
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-628-039-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (314)694-3412
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1545 base pairs
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INFORMATION FOR SEQ ID NO:
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Best Local Similarity 46.55
Matches 195; Conservative
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                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
             STREET: 800 ....
CITY: St. Louis
                                                                                                                                                                                                   OPERATING SYSTEM:
  E: Gary P
800 No.
                                                                                                                                                                                                                                                                                                                                                                                                                             Bond, Gary
                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                              63167
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                                                                                                                                                                                                                         SOFTWARE:
                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-673-388-1
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Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalera
in Bacteria and Plants
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Pred. No. 2.5e-10;
                                                                                         38-21(13585)A
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Clemente, Thomas E.
Connor-Ward, Dannette V.
Fedele, Mary J.
Fry, Joyce E.
Howe, Arlene R.
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Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
Padgette, Stephen R.
Stark, David M.
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Patent No. 5942660
                                         NAME: Bond, Gary
REGISTRATION NUMBER: 29,283
                                                                                  REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3412
                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: DNA (genomic)
US-08-628-039-7
                                                                                                                                                  TELEFAX: (314)695-5435
INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                            6.0%;
FILING DATE: 13-MAR-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 1545 base pairs
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Best Local Similarity 46.5
Matches 195; Conservative
                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                          linear
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APPLICANT: Gruys,
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APPLICANT:
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Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval in Bacteria and Plants
220 ACGGAAGAACAGAAAGCGCACGGCGTGATCACTGCTTCTGCGGGTAACCACGCGCAGGGC 279
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                                                                           211 ACGCCAGAAGAGAGCCCAAAGCCGTAGTTACTCACAGCAGCGGAAACCATGGCCAAGCT
                                                      571 GCTGGAATAGCCATTACAATTAAGGCCCTGAAACCTAGTGTGAAGGTATACGCTGCTGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3: Charles E. Cohen, Monsanto Company,
700 Chesterfield Parkway No. 5958745th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

FILING DATE: 13-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 60.6; DB 2;
Pred. No. 2.5e-10;
0; Mismatches 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Cohen, Charles E. REGISTRATION UNBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(13618)A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    Clemente, Thomas E.
Connor-Ward, Dannette
                                                                                                                                                                                   Sequence 5, Application US/08673388
Patent No. 5958745
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               Padgette, Stephen R. Stark, David M.
                                                                                                                                                                                                                                        Gruys, Kenneth J.
Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                   Hinchee, Maud A. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Howe, Arlene R.
                                                                                                                                                                                                                                                                                                                                                                                                      Fedele, Mary J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1545 base pairs
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Best Local Similarity 46.5
Matches 195; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 63198
COMPUTER READABLE FORM:
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TITLE OF INVENTION:
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Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 13 CLASSIFICATION:
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; MOLECULE TYPE:
US-08-673-388-5
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APPLICANT:
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Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalera
in Bacteria and Plants
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700 Chesterfield Parkway No. 5958745th
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46.5%; Pred. No. 2.5e-10;
Live 0; Mismatches 224;
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                                                                                    Hinchee, Maud A. W.
Clemente, Thomas E.
Connor-Ward, Dannette V.
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                                                  Padgette, Stephen R.
Stark, David M.
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Mitsky, Timothy A.
Kishore, Ganesh M.
                                   Steven C.
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                                                                                                                                             Fedele, Mary J.
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Howe, Arlene R.
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INFORMATION FOR SEQ ID NO:
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Matches 195; Conserv
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Methods of Optimizing Substrate Pools and Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval in Bacteria and Plants
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Pred. No. 2.5e-10;
); Mismatches 224; Indels
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APPLICATION NUMBER: US/08/673,388
FILING DATE: 13-MAR-1996
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Connor-Ward, Dannette
Fedele, Mary J.
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Stark, David M.
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Kishore, Ganesh M.
Slater, Steven C.
  DNA (genomic)
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                                                         Query Match 6.0°
Best Local Similarity 46.5°
Matches 195; Conservative
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NUMBER OF SEQUENCES:
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TITLE OF INVENTION:
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Missouri
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WUMBER OF SEQUENCES: 11
                                                                                                                                                                                                  CCCAACTGCAAGAAACTGGCAATCCAAGCCTATGGAGCATCGATAGTATACTGTGACCCA 390
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ADDRESSEE: Charles E. Cohen, Monsanto Company,
STREET: 700 Chesterfield Parkway No. 5958745th
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NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-21(13618)A
TELECOMMUNICATION INFORMATION:
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FILING DATE: 13-MAR-1996
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Connor-Ward, Dannette V.
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Patent No. 5958745
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Padgette, Stephen R.
Stark, David M.
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Clemente, Thomas E.
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Mitsky, Timothy A.
Kishore, Ganesh M.
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(314)537-6047
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Howe, Arlene R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rozman, Renee J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGIH: 1545 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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APPLICANT: Gruys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 13 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63198
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                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
US-08-673-388-7
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220 ACGGAAGAACAGAAAGCGCACGGCGTGATCACTGCTTCTGCGGGTAACCACGCGCAGGGC 279
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  ADDRESSEE: Charles E. Cohen, Monsanto Company, STREET: 700 Chesterfield Parkway No. 5959179th
                                                                                                                                                                                                                                Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 60.6; DB 2;
Pred. No. 2.5e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                         SOFTWARE: PATENTIN RELEASE #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,877
FILING DATE: 13-MAR-1996
                                                                                                                                                                                                           PC-DOS/MS-DOS
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US-08-614-877-5
Sequence 5, Application US/08614877
Patent No. 5959179
                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38-:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
TELEPHONE: (314)537-6047
                                                                                                                                                                                 IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                          34,565
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APPLICANT: Gruys, Kenneth J.
APPLICANT: Mitsky, Timoth A.
APPLICANT: Kishore, Ganesh A.
APPLICANT: Slater, Steven C.
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nucleic acid
EDNESS: double
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Best Local Similarity 46.5
Matches 195; Conservative
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                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                           OPERATING SYSTEM:
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                                            St. Louis
Missouri
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
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                                                                                                                   63198
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                                                                  STATE: N
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Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalera
in Bacteria and Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 ACGCCAGAAGAAGCCCAAAAGCCGTAGTTACTCACAGCGGGAAACCATGGCCAAGCT 270
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Pred, No. 2.5e-10;
0; Mismatches 224;
                                                                                         38-21(13618)A
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Clemente, Thomas E.
Connor-Ward, Dannette V.
                                                                                  REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
TELEFAX: (314)537-624
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1545 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08614877
                     INFORMATION E. Charles E. 34,565
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Stark, David M.
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Kishore, Ganesh M.
Slater, Steven C.
                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic) US-08-673-388-8
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match 6.0%;
Best Local Similarity 46.5%;
Matches 195; Conservative
                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fedele, Mary J.
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Howe, Arlene R.
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                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
                                                               REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 1
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APPLICANT: Rozman, R
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 5959179 GENERAL INFORMATION:
CLASSIFICATION:
                                               Cohen,
                                                                                                                                                                                                                                                                                                TOPOLOGY:
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APPLICANT:
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                                          NAME:
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Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval in Bacteria and Plants
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                                     580 GCTTGCGTGCGGGTGCTGATCAAACAACTGATGCCGCAAATCAAAGTGATCGCCGTAGA 638
571 GCTGGAATAGCCATTACAATTAAGGCCCTGAAACCTAGTGTGAAGGTATACGCTGCTGA 629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 60.6; DB 2;
Pred. No. 2.5e-10;
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34,565
TE. 38-21(10695)A
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Connor-Ward, Dannette V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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                                                                                                                                 Sequence 7, Application US/08614877
Patent No. 5959179
                                                                                                                                                                                                           Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
Padgette, Stephen R
Stark, David M.
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IBM PC compatible
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                           Hinchee, Maud A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                          Rozman, Renee J
                                                                                                                                                                                                                                                                                                                                                                                  Fry, Joyce E.
Howe, Arlene R.
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(314)537-6047
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                                                                                                                                                                                                                                                                                                                                                                    edele, Mary J
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nucleic acid
EDNESS: double
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MEDIUM TYPE: Floppy
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FILING DATE: 13-MAR
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TITLE OF INVENTION:
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Best Local Similarity
Matches 195; Conserv
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Missouri
                                                                                                                                                                         GENERAL INFORMATION:
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                                                                                                                                                                   Methods of Optimizing Substrate Pools and Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalera in Bacteria and Plants
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                                                                                                                                                                                                                                                                 Charles E. Cohen, Monsanto Company, BB4F
700 Chesterfield Parkway No. 5959179th
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30
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Pred. No. 2.5e-10;
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                                                     Clemente, Thomas E.
Connor-Ward, Dannette V.
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APPLICATION NUMBER: US/08/614,877
FILING DATE: 13-MAR-1996
CLASSIFCATION: 800
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Padgette, Stephen R
                                   Hinchee, Maud A. W. Clemente, Thomas E.
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NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
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FELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
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                                                                                         Fedele, Mary J.
Fry, Joyce E.
Howe, Arlene R.
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Matches 195; Conservative
                   tark, David
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STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
                                                                                     APPLICANT Fedele, M
APPLICANT Fry JOYC
APPLICANT ROZMAN, ARI
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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Missouri
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CITY: S
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  Length 1545;
                                          224; Indels
    DB 2;
                    2.5e-10;
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  Score 60.6;
Pred. No. 2.
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    6.0%;
                                      Matches 195; Conservative
                      Similarity
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in Bacteria and Plants
                                  391 AGTGACGAGTCCAGAGAAAGGTCACTCAAAGAATTATGCAAGAAACAGAAGGCATCTTG 450
                                                                                                                 GTCCATCCCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGAACAATTGCCCTGGAAGTG 510
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13-MAR-1996
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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Kishore, Ganesh M.
Slater, Steven C.
Padgette, Stephen R.
Stark, David M.
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Patent No. 5959179
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Lemente, Thomas E.
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Howe, Arlene R.
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LENGTH: 1545 base pairs
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STRANDEDNESS: double
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COMPUTER READABLE FORM
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TITLE OF INVENTION:
TITLE OF INVENTION:
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STATE: Missouri
COUNTRY: USA
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c). 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-789-300A-2
US-09-134-001C-3876
US-08-403-866-10
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US-08-669-378-6

US-08-669-378-6

US-08-669-378-8

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-09-594-193-7
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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104
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Perfect score:
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Appl Appl Appli Appli Appli Appl Appl Ap			H	09	120	180	240	300	
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		576el Human Pyridoxal Family Member and Us. ,300A 08	DB 4; Leng 168; 15; Indel	OIAGRNLFFKCE : QLTGRNLFFKCE	KLEGIPAYIVVP 	EPAVIAGOGTIA 	DCYQSKLKGELT DCYQSKLKGKLM	GRMKLLIEPTAG ERMKLLIEPTAG	QTVSV 339 : QSVSV 340
3-973-462-25 3-980-115-11 2-273-462-9 3-021-465-73 3-061-465-74 3-062-227-2 3-017-947-2 3-017-947-3 3-484-575A-14 3-484-575A-14 3-484-575A-14 3-484-575A-14 3-484-575A-14 3-484-575A-14 3-484-575A-14 3-484-575A-13 3-477-459-14 3-486-414-14	SINIS	76el Hum Family M 300A 8	e 1582.5; . No. 9.7e- ismatches	TSSILN 	ALTYAA ALTYAA	LVHPNQ : : MVHPNQ	EPSNAD 	ATQLVW ATQLVW	ERPAPY ERPASY
-08-97308-98008-98008-021808-08-66108-08-66308-08-48408-48608-486-	ALIGNMENT	JA 6458576 54789,307789,308 33,208	Score 158 Pred. No.	CHLTPVI 	SSGNHGC	QETEGI :	SVKVYAA 	FEDEIKY 	LNWVGQA : ITWVKQA
US-000000000000000000000000000000000000	~	89300 Ira A No. (t.Enz 15/09, 120 60/18	51	IIQDS : IRDS	WTHS 	TQRI) : : 'AKRV'	ALKPS	VETV	LT-SI LTSS
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212 609 630 947 1416 1642 1642 1642 553 553 553 553 553 553 553 553 553 55		ton US/ Rachel Owen, Depen NUMBER: 2001 NUMBER: 2001 2000-02 3: 4 or Wind	90.9%; / 89.7%; cvative	PADVEKA 	PDTPEEK	OPSDESF IIIIII	(VAGIA) : LAGIA]	VPIIRDI 	INLSGG
N N N N N N		Application Applic	y Match Local Similarity hes 305; Conserva	CAQYCISE CAQYCISE	MAIRGLII : : WAVRSLVI	SASIVYCI 	/PVGGGGA /PVGGGGA	SSIGLNTV	VSPEVKNVCIVLSGGNVDLT-SLNWVGQAERPAPYQTVSV
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		-300A; e. 2, A, No. 641, AND. 641, AND. 641, AND. 641, AND. 671, M. FILLIU APPLICE FILLING F	Match Local Sin es 305;	1 L M	61 LP	121 YO	181 W 181 W	241 KS 241 KS	301 VS
00000000000000000000000000000000000000		RESULT 1 Sequence 2, Application US/09789300A Fatent No. 6458576 GENERAL INFORMATION: APPLICANT: Rudolph-Owen, Laura A. TITLE OF INVENTION: 22406, A No. 64585766 TITLE OF INVENTION: Dependent Enzyme Fant FILE REFERENCE: 35800/208926 CURRENT FILING DATE: 2001-02-20 PRIOR PILICATION NUMBER: US/09/789,30C CURRENT FILING DATE: 2000-02-17 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Mindows Version 4.(C) SEQ ID NO 2 LENGTH: 340 TYPE: PRT CORGANISM: Homo sapiens	Query M Best Lo Matches	Qy Db	Qy . Db	Qy Db	Qy Db	Qy Db	Qy
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PRODUCTION OF L-ISOLEUCINE BY MEANS OF RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE DEHYDRATASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYC----D 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 TFDES-ARAAKAFSQDNDKPFIDPFDDENVIAGQGTVALEIFAQAKKQGISLDKIFVQIG 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210 GGGLIAGITAYSKERYPQTEIIGVEAKGATSMKAAYSAGQ-PVTLEHIDKFADGIAVATV 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 GLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 KAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPE 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 QANIYLKEVVTKTPLQLDPYLSNKYQANIYLKEENLQKVRSFKLRGAYYSISKL---SDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 PSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVP----LVDALVVPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 GGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.7%; SCOLE . 2.9e-...
29.4%; Pred. No. 2.9e-...
''ve 67; Mismatches 145; ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Lactococcus lactis subsp. lactis INDIVIDUAL ISOLATE: ILVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : Foley & Lardner . 3000 K Street, N.W., Suite 500
REGISTRATION NUMBER: 34, 727
REFERENCE/DOCKET NUMBER: 20747/30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1600
TELEFAX: (716) 263-1487
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 2, Application US/08669378
; Patent No. 6107063
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Moeckel, Bettina APPLICANT: Begeling, Lothar APPLICANT: Sahm, Herman TITLE OF INVENTION: PRODUCTION TITLE OF INVENTION: PROCOMBINALITLE OF INVENTION: DEHYDRATAN NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                       : 441 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98; Conservative
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                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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ZIP: 20007-5109
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-403-866-10
                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                            APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS FILLE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-10-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 ALVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIAD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGAS-- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --IVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQV----PLVD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 EIVLIGDTFDHCLAQALNYTKQHKMN-FIDPFNNVYTIAGQGTLAKEILNQAEKEDKTFD 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GVK-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 GASVARVGDITFDIAKDKVDDYVQVDEGAVCSTILDMYSKQAIVAEP-AGALSVSALEQY 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : :||||:::|:: || | |: ||: || |: ||: || |: ||: || |: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||
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Atent No. 5643//>
GENERAL INFORMATION:
APPLICANT: Ehrlich, Stanislav
APPLICANT: Godon, Jean-Jacques
APPLICANT: Renault, Pierre
APPLICANT: Renault, Pierre
TTLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
TTLE OF INVENTION: Synthase from Lactococcus and its applications
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.0%; Score 365; DB 4;
29.8%; Pred. No. 6.6e-32;
tive 60; Mismatches 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 KKQI--ENKTIVCIVSGGNNDINRM 326
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                                        Judgmence 3876, Application US/09134001C Patent No. 6380370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Staphylococcus epidermidis US-09-134-001C-3876
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SYSTEM: PC-DOS/MS-DOS
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Patent No. 5643779
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3876
LENGTH: 424
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nes 97; Conserv
                                    US-09-134-001C-3876
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Matches
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PRODUCTION OF L-ISOLEUCINE BY MEANS OF RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE DEHYDRATASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 LIPDTPEEKPKA-VVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYG--- 122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 GAEVKRVGDLNYTIVEKNOGRVRMMSATEGAVCTEMLDLYONEGIIAEPAGALSIAGLKE 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59; Mismatches 159; Indels
                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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Pred. No. 5.7e-25;
                                                                                                                         PAPLICATION NUMBER: US/08/669,378
CLASSIPICATION A135
CLASSIPICATION A135
PRIOR APPLICATION DATA
APPLICATION DATA
APPLICATION DATA
APPLICATION NUMBER: PCT/DE95/00017
FILING DATE: 09-JAN 1995
PRIOR APPLICATION DATA
APPLICATION NUMBER: DE P 44 00 926.7
FILING DATE: 14-JAN 1994
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                            016881/0142
                                                                   PC-DOS/MS-DOS
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                      MEDLUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
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28.48;
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APPLICANT: Mockel, Bettina
APPLICANT: Eggeling, Lothar
APPLICANT: Sahm, Hermann
                                                                                                                                                                                                                                                                                                                                                                                                                                   (202)672-5300
(202)672-5399
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Matches 95; Conservative
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      COMPUTER READABLE FORM:
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TITLE OF INVENTION:
TITLE OF INVENTION:
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197 HVMVPVGGGGLLAGVVSYMADMAPRTAIVGIEPAGAAS-MQAALHNGGPITLETVDPFVD 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 IRAADIQTAQARISSVIAPTPLQYCPRLSEETGAEIYLKREDLQDVRSYKIRGALNS--- 77
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                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 016881/0142
TELECOMMUNICATION INFORMATION:
TELEBONE: (202)672-5399
TELEX: 904134
                                                          PRIOR APPLICATION DATA: PCT/DE95/00017
APPLICATION NUMBER: PCT/DE95/00017
FILING DATE: 09-JAN-1995
PRIOR APPLICATION DATA: DE P 44 00 926.7
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US/08/669,378 FILING DATE: 20-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Application US/08669378
Patent No. 6107063
GENERAL INFORMATION:
APPLICANT: Moeckel, Bettina
APPLICANT: Eggeling, Lothar
APPLICANT: Sahm, Hermann
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Best Local Similarity 28.18;
Matches 94; Conservative
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                                                                                                                                                                                                                NAME: Bent, Stephen A. REGISTRATION NUMBER: 2
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: protein
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & L.
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TITLE OF INVENTION:
TITLE OF INVENTION:
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STATE: D.C.
                    FILING DATE: 20 CLASSIFICATION:
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PRODUCTION OF L-ISOLEUCINE BY MEANS OF RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE DEHYDRAIASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     239 GVK-SSIGLNTWP11RDLVDDVFTVTEDEIKYATQL--VWGRMKLLIEPTAGVALAAVLS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 GAEVKRVGDLNYTIVEKNOGRVHMMSATEGAVCTEMLDLYONEGIIAEPAGALSIAGLKE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ::||||||||::||: : | : ||: | |: |
197 HVMVPVGGGGLLAGVVSYMADMAPRTAIVGIEPAGAAS-MQAALHNGGPITLETVDPFVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  78 -GAOSPOEORDAGIVAASAGNHAQGVAYVCKSLGVQGRIYVPVOTPKOKRDRIMVHGGEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
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28.1%; Pred. No. 7.3e-25;
ive 60; Mismatches 159; Indels
                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                        1: Foley & Lardner
3000 K Street, N.W., Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE95/00017
FILING DATE: 09-7AN-1995
PRIOR APPLICATION DATA:
PRICKTON NUMBER: DE P 44 00 926.7
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 016881/0142
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/669;378
FILING DATE: 20-MAR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: (202)672-5300
                                                                                                                                                                                                                                                                                                      Floppy disk
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Best Local Similarity 28.13
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Bent, Stephen A. REGISTRATION NUMBER: 2
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
            TITLE OF INVENTION: PROOF TITLE OF INVENTION: RECCTITLE OF INVENTION: DEHNUMBER OF SEQUENCES: 18 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                     ZIP: 2007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                      Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                              STATE: D.C
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                                                                                                                                          ADDRESSEE:
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                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 ASIVYCDPSDESREKVÏQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLV---D 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 GAEVKRVGDLNYTIVEKNQGRVHMMSATEGAVCTEMLDLYQNEGIIAEPAGALSIAGLKE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78 -GAOSPQEQRDAGIVAASAGNHAQGVAYVCKSLGVQGRIYVPVQTPKQKRDRIMVHGGEF 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 ALVVPVGGGGWVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIAD 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 IRAADIQTAQARISSVIAPTPLQYCPRLSEETGAEIYLKREDLQDVRSYKIRGALNS--- 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.4%; Score 302; DB 3; Length 436; Best Local Similarity 28.1%; Pred. No. 7.3e-25; Matches 94; Conservative 60; Mismatches 159; Indels
                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,378 FILING DATE: 20-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 QHFQTVSPEVKNVCIVLSGGNVDLTSLNWVGQAER 330
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PRIOR APPLICATION DATA:
PAPLICATION NUMBER: PCT/DE95/00017
FILING DATE: 09-JAN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 00 926.7
FILING DATE: 14-JAN 1994
ATTORNEY/AGENT INFORMATION:
                     Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 016881/0142
                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6107063
GENERAL INFORMATION
APPLICANT: Moeckel, Bettina
APPLICANT: Eggeling, Lothar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 0168
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEFAX: 904136
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29,768
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amino acid
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       STREET: 3000
CITY: Washington
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                                                                                     COUNTRY:
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296 OHFOTVSPEVKNVCIVLSGGNVDLTSLNWVGQAER 330
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REFERENCE/DOCKET NUMBER: 016881/0142
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/OR /fc/ 1-7-
                                                                                                                                 ; Sequence 8, Application US/08669378 ; Patent No. 6107063
                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Mocckel, Bettina
APPLICANT: Segeling, Lothar
APPLICANT: Salm, Hermann
TITLE OF INVENTION: RECOMBINA
TITLE OF INVENTION: BETOMBINA
TITLE OF INVENTION: BETOMBINA
TITLE OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       STATE: USA
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
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28.9%;
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amino acid
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Best Local Similarity 28.99
Matches 97; Conservative
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INFORMATION FOR SEQ ID NO:
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                                                                                                             US-08-669-378-8
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                                                                                                                           PRODUCTION OF L-ISOLEUCINE BY MEANS OF RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE DEHYDRATASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   137 VSLVVTGNNFDEASAAAHEDAERTGATLIEPFDARNTVIGQGTVAAEILSQLTSMGKSAD 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99
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21 IRAADIQTAQARISSVIAPTPLQYCPRLSEETGAEIYLKREDLQDVRSYKIRGALNS---
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                                                                                                                                                                                                                                                                                                                                     COMPUTER READON JION JUNE MEDIUM TYPE: Floppy disk COMPUTER: Floppy disk COMPUTER: TBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 CURREWT APPLICATION NOATA: US/08/669,378 FILING DATE: 20-MAR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 7.3e-25; 
; Mismatches 159;
                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE95/00017
FILING DATE: 09-JAN 1995
PRIOR APPLICATION DATA: DE P 44 00 926.7
FILING DATE: 14-JAN 1994
ATTORNEY/AGENT INFORMATION:
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           Sequence 10, Application US/08669378 Patent No. 6107063 GENERAL INFORMATION:
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                                                               APPLICANT: Moeckel, Bettina
APPLICANT: Eggeling, Lothar
APPLICANT: Sahm, Hermann
TITLE OF INVENTION: PRODUCTION
TITLE OF INVENTION: RECOMBINAN
TITLE OF INVENTION: DEHYDRATAS
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TELECOMMUNICATION INFORMATION:
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X: (202)672-5399
904136
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Bent, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 17.4'
Best Local Similarity 28.1'
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-669-378-10
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       NUMBER OF SEQUENCES:
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PRODUCTION OF L-ISOLEUCINE BY MEANS OF RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE DEHYDRATASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 ASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLV---D 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 LIPDTPEEKPKA-VVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYG--- 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   179 ALVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIAD 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 300; DB 3; Length 436; Pred. No. 1.2e-24; 58; Mismatches 157; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
316 MSF---APGSVVVCII-SGGNNDV--LRYAEIAER 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: PCT/DE95/00017
FILING DATE: 09-JAN-1995
PRIOR APPLICATION NUMBER: DE P 44 00 926.7
APPLICATION NUMBER: DE P 44 00 926.7
ATONNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                             E: Foley & Lardner
3000 K Street, N.W., Suite 500
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197 HVMVPVGGGGLLAGVVSYMADMAPRTAIVGIEPAGAAS-MQAALHNGGPITLETVDPFVD 255
                                     239 G--VKSSIGLNTWPIIRDLVDDVFTVTEDEIKYATQL--VWGRMKLLIEPTAGVALAAVL 294
                                                                          256 GGEVKRVGDLN-YTIVEKNQGRVHMMSATEGAVCTEMLDLYQNEGIIAEPAGALSIAGLK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----RGLIPDTPE-EKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLA- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KLGKKGGIVPGTVQVESKTTIIEPTSGNTGIALAAAALLGLKCTIVMPATDTSREKRAQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----IA 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----TWPIIRDL-----VDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQ 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 KVIGVEPEGS-AVLSGSLKATLILAGKPGPLHGRDSKYLLQDEPVTLPETKSIGIGLGVP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19 IQDSIHLTPVLTSSILNQIAGRNL-----FFKCE-LFQKTGSFKIRG-ALNAI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 GQGTIALEVLNQV-----PLVDALVVPVGGGGMVAGIAITIKALKPS-----V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                205 KVYAAEPSNADDCYQSKLKGELT----PN-LH------PPETIADGVKSSIGLN--
                                                                                                                                                                                                                                                                                               APPLICANT: Meyers, Rachel
APPLICANT: Meyers, Rachel
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate
TITLE OF INVENTION: Dependent Enzyme Family Member and Uses Therefore
FILE REFERENCE: 35800/208926
CURRENT APPLICATION NUMBER: US/09,7789,300A
PRIOR APPLICATION NUMBER: US 60/183,208
PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Pyridoxal-Phosphate Dependent Enzyme Family Domain OTHER INFORMATION: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQAYGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                             295 SQHFQTVSPEVKNVCIVLSGGNVDLTSLNWVGQAER 330
                                                                                                                                     17.0%; Score 296.5; DB 4; 30.2%; Pred. No. 2.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               297 HFQTVSP--EVKNVCIVLSGG 315
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358 AKEGKKPLNKGKTIVVILSGG 378
                                                                                                                                                                                                                                             Sequence 4, Application US/09789300A Patent No. 6458576 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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Matches 115; Conserv
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SEQ ID NO 4
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US-09-088-435-1 ; Sequence 1, Application US/09088435 ; Patent No. 6277619

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127 AQELAKRDGWEN----VPPFDHPLIWKGHASLVQELKAVLRTPP--GALVLAVGGGGLLA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 GIAITIKAL----KPSVKVYAAEPSNADDCYQSKL-KGELTPNLHPPETIAD--GVKSSI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 VVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYC----DPSDES 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135 REKVTQRIMQETEGILVHPNQEPAVIAGQGTIALE---VLNQVPLVDALVVPVGGGGMVA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    245 GLNT-------WPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAG-VALAA 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 QDSIH-LTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPKA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 325;
                                         APPLICANT: PATTERSON, CHANDRA
TITLE OF INVENTION: SERINE DEHYDRATASE HOMOLOG
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 14.6%; Score 254.5; DB 4 Best Local Similarity 28.1%; Pred. No. 8.8e-20; Matches 92; Conservative 59; Mismatches 117
                                                                                                                                                                                                                                                                                                                  SYSTEM: Windows
FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293 VLSQHFQT---VSPEVKNVCIVLSGGN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 GLLRRLQAEGCLPPSLTSVVVIVCGGN 308
                                                                                                                        3: Incyte Pharmaceuticals,
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                 US/09/088,435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                            IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 325 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEO ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      650-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: THP1A:
CLONE: 2752518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                   94304
                                                                                                                                                                                            CA
                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                COMPUTER:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                          SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-088-435-1
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264 IARKLKEKCPGCRIIGVDP------EGSI---LAEPEELNQTEQTTYEVEGIGYD 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 EPTSGNTGIGLALAAAVRGYRCIIVMPEKMSSEKVDVLRALGAEIVRTPTNARFDSPESH 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EKVTQRIMQE--TEGILVHPNQEPAVIAGQGTIALEVLNQVP-LVDALVVPVGGGGMVAG 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81 THSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCD-----PSDESR 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 TPVLTSSILNQIAGR-----NLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPKAVV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26 TPVLTSSILNQIAGR----NLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPKAVV 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           248 TWPII--RDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAG--VALAAVLSQHFQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Yuan, Chong
TITLE OF INVENTIONS METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25889-1651
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PALENTIN VET: 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 185.5; DB 1;
; Pred. No. 1e-11;
43; Mismatches 133;
...к: US/08/120,960
12-SEP-1993
18: 424
                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: PEPPER PH.D., FREDERICK W.
REGISTRATION NUMBER: 31,286
TELEPORMUNICATION INFORMATION:
TELEPHONE: 619-546-4410
TELEPAX: 619-453-2839
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-347-878-9; Sequence 9, Application US/09347878C; Patent No. 6376210; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.7%;
Best Local Similarity 27.4%;
Matches 81; Conservative 4
                                                                                                                                                                                                                                                                                         : 551 amino acids
amino acid
            CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein US-08-120-960-2
                             APPLICATION NUMBER:
FILING DATE: 12-SEI
CLASSIFICATION: 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Homo sapiens US-09-347-878-9
                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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LENGTH: 551
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                                                                                                                GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: BYDIBERNIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BYDIBERNIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-108-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         86 N-HGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQA--YGASIVYCDPSDESREKVTQRI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 MQETEGILVHPNQEPAVIAGQGTIALEVLNQV--PLVDALVVPVGGGGMVAG----IAI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218 HNKKNTQLPQMFGFQAEGASPIVQNKI-----IKNPETIATAIR--IGNPASWQKAVN 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              255 LVDD----VFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVKNVCI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         196 TIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSSIG-LNTWPIIRD 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 TPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPKAVVTHSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44 TPLIYCENLSQKLDIELYVKYEGANPTGSFKDRGMVMA----VTKAKEQGKKVVICASTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.2%; Score 229; DB 4; Length 367; Best Local Similarity 26.0%; Pred. No. 7.5e-17; Matches 86; Conservative 66; Mismatches 147; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICAMY: KRAUS, JAN P
TITLE OF INVENTION: DNA SEQUENCE ENCODING HUMAN
TITLE OF INVENTION: CYSTATHIONINE B-SYNTHASE
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: 11MORTH 6 BARRESE
STREET: 4350 LA JOLLA VILLAGE DRIVE, SUITE 300
CITY: SAN DIEGO
STATE: CALLFORNIA
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 ILTGNGLKDPDTAISLLDNPIQPLPNNKESI 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           311 VLSGGNV--DLTSLNWVGQAERPAPYQTVSV 339
                                                                         Sequence 4168, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08120960 Patent No. 5523225 GENERAL INFORMATION:
                             RESULT 12
US-09-134-001C-4168,
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GENERAL INFORMATION:

APPLICAMY: Lynn Doucette-Stamm et al
ATILLE OF INVENTION: DEIDEMAIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007

CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-108

PRIOR FILING DATE: 1997-108

RIOR FILING DATE: 1997-108

RIOR FILING DATE: 1997-08-14

NUMBER: OF SEQ ID NOS: 5674

LENGTH: 312
                                                                                                                                                                                                                                                                                        136 EKVTQRIMQE--TEGILVHPNQEPAVIAGQGTIALEVLNQVP-LVDALVVPVGGGGMVAG 192
                                                                                                                                                                                                     193 IAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSS----IGLN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 VVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPSDESREKV 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSSIGLNTWP--I 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           190 AQHLKTY--DVKNYIVEPEG-----SVLNGGVS---HPHAT-----EGIGSEKWPSFL 232
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                                                                                                  204 VGVAWRLKNEIPNSHILDQYRNASNPLAHYDTTADEILQQCDGKLDMLVASVGTGGTITG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DSIHLTPVLTSSILNQIAGRN--LFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPKA 78
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                                                                                                                                                                                                                                                                                                                                                                                                                      248 TWPII---RDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAG--VALAAVLSQHFQ 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3920, Application US/09134001C
Patent No. 6380370
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US-09-134-001C-3920
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Search completed: June 24, 2003, 05:36:43 Job time : 44.4683 secs

7 491.8 48.1 667 10 BB609829 B	410.4 40.1 1159 14 BQ215405 402.4 39.3 918 14 BQ885621 391.8 38.3 823 13 BI738966 383 37.4 391 14 BQ303565	380.6 37.2 404 14 B0303568 379.6 37.1 386 14 B0303566 376.6 36.8 698 9 AV022510 365.4 35.7 455 9 AI322578	35.3 35.6 602 10 AV37491 352.8 34.5 471 14 H73097 348.6 34.1 729 13 BG965678	341 33.3 394 10 AV649514 337 32.9 793 12 BG404240	329 32.2 /42 9 A132530/ 328.2 32.1 827 13 B1332919 323 8 31 7 426 14 B6748	321.0 31.4 519 10 BB641631 320.8 31.4 830 12 BP135412 316.3 0.0 666 17 BP135412	215.1 20.0 20.0 10 BB052400 300.2 29.3 380 9 AA034539 299 29.2 661 10 BB621410 295.4 28.9 688 10 BB625125	205:0 20:0 109 12 BE532321 28:2 27:6 544 9 AA432108 274:6 26:9 645 10 AW211242 274:6 26:8 646 10 BB644584 274 26:8 566 14 BM766119	273 26.7 288 266.4 26.0 632 266.2 26.0 611 265.4 25.9 672 258.2 25.2 672	255.6 25.0 426 14 D53895	ALIONADIA.	AK017235 LOCUS AK017235 LOCUS AK017235	1372 1:C57BL/6J) adult male pituitary N full-length enriched mouse cDN	ORGANISM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. REFERENCE 1 AUTHORS Carninci,P. and Hayashizaki,Y.		MEFERENCE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., AUTHORS Carninci, P., Shibata, Y., Muramatsu, M. and Hayashizaki, Y. Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes JOURNAL Genome Res. 10 (10), 1617-1630 (2000) MEDLINE 20499374 PUBMED 11042159
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd. OM nucleic - nucleic search, using sw model	<pre>Run on: June 24, 2003, 07:02:30 ; Search time 1462 Seconds</pre>	Title: US-09-889-609B-9 Perfect score: 1023 Sequence: 1 atgtggctcagtattgcatatcagtctgtttctgtttaa 1023	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 16154066 segs, 8097743376 residues	Total number of hits satisfying chosen parameters: 32308132	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries		<pre>4: em_estmu:* 5: em_estov:* 6: em_estp1:* 7: em_estp0:* 8: em_htc:*</pre>		13: 95_est4:* 14: 9b_est5:* 15: em_estfun:*	16: em_estom:* 17: gb_gss:* 18: em_gss_bum:* 19: em_gss_inv:*	20: em_gss_pln:* 21: em_gss_tvrt:* 22: em_gss_tun:* 23: em_gss_mam:* 24: em_gss_mam:* 25: em_gss_other:* 26: em_gss_pro:*	27: em_gss_rod:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	RIES	2 751 73.4 78.5 1398 11 2 72.7 73.4 78.5 1398 11 3 729.2 71.3 848 9 4 602 58.8 634 14 5 526 51.4 527 9 5 528 51.2 769 12

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CDNA was cleaved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="pituitary gland"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="adult"
1. .1398
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                                                    with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       291 ATGTGTGCTCAGTACTGCATCTCCTTTGCTGATGTTGAAAAAGCTCATATCAACATTCAA
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashinco,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Yoneda,Y., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer 20530913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGAGACTTTTTTTTTTTTTTVN 3'1, cDNA was prepared by using trehalose thermo-activated reverse transcriptuse and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 3.0 and subtraction to adapter of sequence [5' and conditions of the primer adapter of sequence [5' and conditions of the primer adapter of sequence [5' and conditions of con
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 023. Note: this is a NIH_MGC Library." BASE COUNT 225 a 168 c 200 g 192 t C. ORIGIN	rry Match 73.4%; Score 7 tt Local Similarity 99.6%; Pred. Precent Cohes 784; Conservative 0; Misn	Oy 104 ATCAACTAACAGGCGCAATCTTTTCTTCAAATGTGAACTCTTCCAGAAAACAGGATCTT 163	Qy 164 -TTAAGATTCGTGGTGCTCTCAATGCCGTCAGAAGCTTGGTTCCTGATGCTTTAGAAAGG 222	Oy 223 AAGCCGAAAGCTGTTGTTACTCACAGCAGGAAACCATGGCCAGGCTCTCACCTATGCT 282	Oy 283 GCCAAATTGGAAGGAATTCCTGCTTATATTGTGGTGCCCAGACAGCTCCAGACTGTAAA 342	Qy 343 AAACTTGCAATACAAGCCTACGGAGCGTCAATTGTATACTGTGAACCTAGTGATGAGTCC 402	QY 403 AGAGAAATGTTGCAAAAGATTACAGAAGAAACAGAAGGCATCATGGTACATCCCAAC 462 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		Qy 583 ATTACAGTTAAGGCTCTGAAACCTAGTGTGAAGGTATATGCTGCTGAACCCTCAAATGCA 642	Db 54.0 GATGACTGCTACCAGCTGAAGGGGAAACTGATGCCCAATCTTTATCCTCCAGA 599	QY 763 CTTGTGGATGATATCTTCACTGTCACAGGGATGAAATTAAGTGTGCAACCCAGCTGGTG 822 .	823 TGGGAGAGGA 719 TGGGAGAGGA	OY 883 TCTCAAC 889 Db 779 TCTCAAC 785	RESULT 3 AU131397 LOCUS AU131397 AU131397 AU131397 AU131307 AU1313
Db 890 AAACCTAGTGTGAAGGTATACGCTGCTGAGCCCTCGAATGCAGATGACTGCTACCAGTCT 949 Qy 661 AACTGAAGGGAAACTGATGCCCAATCTTTATCCTCCAGAAACCATAGCAGTGTGT 720 Db 950 AAATGAAAGGAAAACTGACCCCAATCTTCATCTCCAGAAACCAATGCTGTC 1009	AAATCCAGCATTGGCTTGAACACCTGGCCTATTATCAGGGACCTTGTGGGATGATCTTC 780	OY 781 ACTGTCACAGAGGAAATTAAGTGTGCAACCCAGCTGGTGGGGAGGAGGATGAAACTA 840	OY 841 CTCATTGAACCTACAGCTGGTGTTGGAGTGCTGTGTGTGT	OY 901 GTTTCCCAGAAGTAAAGAACATTGTATTGTGTCCTCAGTGGTGGAAATGTAGACTTAACC 960 11	QY 961 TCCTCCATAACTTGGGTGAAGCAGGCTGAAAGGCCAGCTTCTTATCAGTCTGTTTCTGTT 1020	OY 1021 TAA 1023 Db 1307 TAA 1309	RESULT 2 BI763753 BI763753 785 bp mRNA linear EST 25-SEP-2001 DEFINITION 603047780F1 NIH_MGC_116 Homo sapiens CDNA clone IMAGE:5188099 5',		EUKATYOLG MELAZOA; CHOTOALA; VERTEPRATA; EULGLEOSCOMI; REFERENCE 1 (Dasses 1 to 785) AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE NALIONAl Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D.	ک	found through the I.M.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM1169 row: p column: 20 High quality sequence stop: 783.	FEATURES Location/Qualifiers source 1. 785 /organism="Homo sapiens" /db_xref="taxor.9606"	. kidnev. stomach. Ve	pCMV-SPORT6; Site_1: Not1; Site_2: ECORV (destroyed); RNA source anonymous pool of 3 colons, age 26 yo male, 49 yo female, 71 yo male colon; 46 yo male kidney, and pool of 2 stomachs, 62 yo male and 70 yo female. Library is oligo-dT primed and directionally cloned (EcoRV site is

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/note="Vector: pMEIDSFL5; mRNA from NT2 neuronal precursor cells after 2 vecks retinoic acid (RA) induction"
187 c 214 g 207 t 4 others
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                                     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 848)
                                                                                                                                                                                                                                       Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
                                                                                         Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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                                                                                                                                             Unpublished (2000)
Contact: Takkon Isogai
Connics: Takboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Fax: 81-438-52-3975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.3%; Score 729.2; DB 9;
llarity 98.0%; Pred. No. 6.4e-208;
Conservative 0; Mismatches 12;
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Program for Rat Gene Discovery and Mapping
University of lowa
451 Eckstein Medical Research Building lowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 8256
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com)
Seg primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BM719814 634.bp mRNA linear EST 01-MAR-2002 UI-E-EJO-ahu-j-16-0-UI.rl UI-E-EJO Homo sapiens cDNA clone UI-E-EJO-ahu-j-16-0-UI 5', mRNA sequence.
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/lab_host="PH10B (Life Technologies) (TI phage resistant)"
/note="corgan: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-E-EJ0 is a subtracted cDNA library constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
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                                 GTGGTACCTGTAGGTGGAGGAGGAATGCTTGCTGGAATAGCAATTACAGTTAAGGCTCTG
                                                                                                                                                                                                                                                                                   AAGCTGAAGGGGAAACTGATGCCCAATCTTTATCCTCCAGAAACCATAGCAGATGGTGTC
                                                                                                                                         AAACCTAGTGAAGGTATATGCTGCTGAACCCTCAAATGCAGATGACTGCTACCAGTCC
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases I to 527) Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Washu-Merck EST Project 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pT7T3D-Pac (Pharmacia) with a modified bolylinker; Site_1: Not I: Site_2: Eco RI: 1st strand cDNA was prepared from mRNA obtained from pooled 8-9 week (total) fetus ameterial with a Not I - oligo(dT) primer [5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 TCCATTTTGAATCAACTAACAGGGGGGCAATCTTTTCTTCAAATGTGAACTCTTCCAGAAA 153
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                                                                                                                                                                                                                                                                                       rough LLNL ; contact the for further information.
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Pred. No. 7e-147;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="Soares_total_fetus_Nb2HF8_9w"
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/lab_host="DH108"
                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL
IMAGE Consortium (info@image.llnl.gov) for further
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 496.
Location/Qualifiers
                                                                                                                                                                                                                 4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
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/db_xref="GDB:5981773"
/db_xref="taxon:9606"
/clone="IMAGE:784155"
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100.0%; Pr
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stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (GT)18 tail. The sequence tags for this library are: fetal eyes, AGAATCAAGA; lens, CGATTAAGCGA, centina, CGGCG, Retina Foveal and Macular, GTCC; RPE and Choroid, ACCTA. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTAGACTTAACCTCCACATAACTTGGGTGAAGCAGGCTGAAAGGCCCAGCTTCTTATCAG 1008
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IMAGE:784155 5' similar to SW:YKV8_YEAST P36007 HYPOTHETICAL 34.9
KD PROTEIN IN FRE2-JEN1 INTERGENIC REGION. ;, mRNA sequence.
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Ackawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishi, Y., Ito, M., Kawai, J., Konda, M., Kawai, J., Konno, H., Kouda, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Koya, S., Matsuyama, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shibata, K
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days embryo Mus musculus
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
C.M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
                                                                                                                                       CTACGGAGCGTCAATTGTATACTGTGAACCTAGTGATGAGTCCAGAGAAAATGTTGCAAA 419
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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     GAAACCTAGTGAAGGTATATGCTGCTGAACCCTCAAATGCAGATGACTGCTACCAGTC
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BF163794
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  CATCCCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGGACAATTGCCCTGGAAGTGCTG 513
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                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 769)
NIH-WGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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/strain="c2ECH II"
/db_xref="taxon:10090"
/clone="IMAGE:3988873"
/clone_lib="NCI_CGAP_Lu29"
/tissue_type="spontaneous tumor, metastatic to mammary.
Stem cell origin "
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo d Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM9198 row: a column: 02

High quality sequence stop: 699.

Location/Qualifiers
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Pred. No. 3.8e-146;
0; Mismatches 87; Indels
                                                                                                                                  514 AACCAGGTTCCTTTGGTGGATGCACTGGTGGTACCTGTAGGTGGAG
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Best Local Similarity 87.1%;
Matches 633; Conservative
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 652)

1 (bases 1 to 652)

2 Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Fu, G., Rang, Y., Chen, Z., Cang, L., Xu, S., Can, M., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Chen, J., Chen, Z. and Han, Z.

L Unpublished (2000)

Contact: Zeguang Han

Chinese National Human Genome Center at Shanghai

351 Guo Shoujing Road, Zhangjiang HI-Tech Park, Pudong, Shanghai

Tel: 86-21-50801922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AV709023 ADC Homo sapiens cDNA clone ADCAUC06 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                     116 GATTCTATCCACCTCACACCAGTGCTAACAAGCTCCATTTTGAATCAACTAACAGGGGG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 AATCTTTTCTTCAAATGTGAACTCTTCCAGAAAACAGGATCTTTTAAGATTCGTGGTGCT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                                      518 GCTGGACAAGGACAATTGCCCTGGAAGTGCTGAACCAGGTTCCCTTGGTAGATGCACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GATTCTATCCACCTCACACCAGTGCTAACAAGCTCCATTTTGAATCAACTAACAGGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGAGTTACAGAAGAAACAGAAGGCATCATGGTACATCCCAACCAGGAGCCTGCAGTGATA
                                                                                                                                                                                                                                                 481 GCTGGACAAGGGACAATTGCCCTGGAAGTGCTGAACCAGGTTCCTTTGGTGGATGCACTG
                                                                                                                                                                                                                                                                                                                                                          541 GTGGTACCTGTAGGTGGAGGAGGAATGCTTGCTGGAATAGCAATTACAGTTAAGGCTCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: hanzg@chgc.sh.cn .
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 487.6; DB 10;
Pred. No. 2.8e-135;
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/dev_stage="Adult"
/lab_host="SOLR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="ADCAUC06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 9
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(VII), 1757-1771 (2001)

(VIII), 
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genes. Genome Res. . 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GATTCTATCCACCTCACCAGTGCTAACAAGCTCCATTTTGAATCAACTAACAGGGCGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                   Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="1190028F16"
/clone_lib="RIKEN full-length enriched, 18 days embryo"
/dev_stage="18 days embryo"
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Pred. No. 1.5e-136;
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88.7%;
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                                                                                                                              Site_2:
                                                                                                   cancerous liver tissue"
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                                                                                                                                                                                                                                              GATTCTATCCACCTCACACCAGTGCTAACAAGCTCCATTTTGAATCAACTAACAGGGCGC
                                                                                                                                                                                                                                                                                  AATCTTTTCTTCAAATGTGAACTCTTCCAGAAAACAGGATCTTTTAAGATTCGTGGTGCT
                                                                                                                                                                                                                                                                                           CTCAATGCCGTCAGAAGCTTGGTTCCTGATGCTTTAGAAAGGAAGCCGAAAGCTGTTGTT
                                                                                                                                                                                                                                                                                                                                AGAGTTACAGAAGAAACAGAAGGCATCATGGTACATCCCAACCAGGGGCCTGCAGTGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----ACCAGGAGCTGCAGATAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      481 GCTGGACAAGGGACAATTGCCCTGGAAGTGCTGAACCAGGTTCCTTTGGTGGATGCACTG
                                                                                                                                                                                           58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ECORI;
                                                                                                                                                                          Length 697;
                                                                                                                           /note="Vector: pBluescript sk(-); Site_1:
                                                                                                                                                                                           Indels
201203, P. R. China
TTel: 86-21-50801919(ex.45)
Fax: 86-21-50801925.
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
                                                                                                                                                                  Score 479.2; DB 10;
Pred. No. 9.5e-133;
                                                                                                  /tissue_type="corresponding non
/dev_stage="Adult"
/lab_host="SOLR"
                                                                                                                                               u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGCTGAAGGGGAAACTGATGCCCAATCTT 690
                                                                                                                                                                                         0; Mismatches
                                                                                                                                               171
                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="GLCBSF06"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGCTTGAAGGGAAACTGATGCCCAACTTT
                                             Location/Qualifiers
                                                                                                                                                δ
                                                                                                                                                174
                                                                                        clone_lib="GLC"
                                                                                                                                                                        46.8%;
87.1%;
                                                                                                                                               154 c
                                                                                                                                                                                          601; Conservative
                                                                                                                                                                                   Similarity
                                                                                                                                              190
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Best Local
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RESULT

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819 bp mRNA linear EST 20-SEP-2001
NIH_MGC_94 Mus musculus cDNA clone IMAGE:5367042 5',
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCAATGCCGTCAGAAGCTTGGTTCCTGATGCTTTAGAAAGGAAGCCGAAAGCTGTTGTT 240
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="retina"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                   Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTGCTTATATTGTGGTGCCCCAGACAGCTCCAGACTGTAAAAAACTTGCAATACAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGTGTGCTCAGTATTGCATCTCCTTTGCTGATGTTGAAAAAGCTCATATCAACATTCGA
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                                                                                                                                                                                                                                1 (bases 1 to 819)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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89.0%; Pred. No. 3.1e-124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ite: LLAMI1933 row: p column: 19
th quality sequence stop: 817.
Location/Qualifiers
1. 819
/organism="mus musculus"
/db_xref="taxon:10090"
/clone="ImmGE:5367042"
/clone="lib="NIH_MGC_94"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
                                                                                            GI:15716056
                                                                                                                                                                                                                                                                                                           Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 487; Conservative
                                            mRNA sequence.
BI739030
                                                                                                                                                                  Mus musculus
                      603359880F1
                                                                                                                                              house mouse
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697

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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE

MEDLINE COMMENT

JOURNAL

DEFINITION

ACCESSION

RESULT 12 BE655084

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1159 bp mRNA. linear EST 02-MAY-2002
AGENCOURT_7558931 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6045236
5', mRNA sequence.
BQ215405
                                                                                                                                                                                                                               AGGTTCCCTTGGTAGATGCACTGGTGGTACCAGTAGGAGGAGGAGGAATGGTTGCTGGAA 120
                                                                                                                                                                  121 TAGCCATTACAATTAAGGCCCTGAAACCTAGTGTGAAGGTATACGCTGCTGAGCCCTCGA 180
                                                                                                                                                                                                                                                                                          CAGAAACCATAGCAGATGGTGTCAAATCCAGCATTGGCTTGAACACCTGGCCTATTATCA 757
                                                                                                                                                                                                                                                                                                               TGGTGTGGGAGAGGATGAACTACTCATTGAACCTACAGCTGGTGTTGGAGTGGCTGCTG 877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCTGTCTCAACATTTTCAAACTGTTTCCCCAGAAGTAAAGAACATTGTATTGTGCTCA 937
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1159)
NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Sträusberg, Ph.D.
1 CCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGAACAATTGCCCTGGAAGTGCTGAACC
                                       GGGACCTTGTGGATATCTTCACTGTCACAGAGGATGAAATTAAGTGTGCAACCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov row: b column: 21
                                                                                                                         TAGCAATTACAGTTAAGGCTCTGAAACCTAGTGTGAAGGTATATGCTGCTGAACCCTCAA
                                                                                                                                                                                                            ATGCAGATGACTGCTACCAGTCCAAGCTGAAGGGGAAACTGATGCCCAATCTTTATCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6045236"
/clone_lib="NIH_MGC_92"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BQ215405.1 GI:20396805
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JOURNAL
COMMENT
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AUTHORS
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BQ215405
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NH=BMAP_MCO_N"
/dev.stage="127-32 days"
/dev.stage="127-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified
Polylinker; Site_l: Not I; Site_2: Eco RI; The
polylinker; Site_l: Not I; Site_2: Eco RI; The
polylinker; Cartex or a normalized library constructed
from mouse cortex. The tag is a string of 5 nucleotides
present between the Not I site and the oligo-dr track.
The library was constructed as described by Bonaldo,
Lennon and Soares, Genome Research 6: 791-806, 1996.
Tissue provided by Ms. Annie Novakovich, Zivic-Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mEST@mail.nih.gov

CDNA Library Preparation: M.B. Soares Lab Clone distribution:

Researchers may obtain BMAP CDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP CDNAS whose availability will be considered under appropriate and limited collaborative arrangements

Seq primer: M13 Reverse.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 565)

Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                               AGAGTTACAGAAGAAACAGAAGGCATCATGGTACATCCCAACCAGGAGCCTGCAGTGATA
                                       CCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGGACAATTGCCCTGGAAGTGCTGAACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   National Institute of Mental Health
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda,
20892-9643, USA
TEL: 301 443 1706
Fax: 301 443 9890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 10; Length 565;
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44.1%; Score 450.8; DB 10;
Best Local Similarity 88.5%; Pred. No. 3e-124;
Matches 501; Conservative 0; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/clone="UI-M-AL1-ahr-f-12-0-UI"
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97044477
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                                                                                                                                                                                                            GTGGTAC 819
                                                                                                                                                                                    GTGGTAC 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                             house mouse,
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FEATURES

BASE COUNT ORIGIN

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BI738966 823 bp mRNA linear EST.20-SEP-2001 603359780F1 NIH_MGC_94 Mus musculus cDNA clone IMAGE:5367043 5',
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov
Plate: LLAM13790 row: h column: 08
High quality sequence stop: 609.
Location/Qualifiers
L. 918
/ Organism="Mus musculus"
/ Ab_xref="taxon: 10090"
/ Clone="linAGE: 6332599"
/ Clone="line" lluAGE: 6332599"
/ Clone="line" lluAGE: 6332599"
/ Clone="line" lluAGE: 6332599"
/ Rote="Organ: otocysts: Vector: pcWv-SPORT6.1.ccdb;
/ Iab_host="DHIOB (phage-resistant)"
/ Iab_host="DHIOB (phage-resistant)"
/ Site_l: EcoRvy: Site_l: Not1; Cloned unidirectionally.
Primer: Oligo dT. Average insert size 1.95 kb.
Constructed by ResGen, Invitrogen Corp. Note: this is a
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Pred. No. 1.4e-109;
0; Mismatches 92;
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Rodentia; Sciurognathi; Muridae; Murinae; Mus
/lab_host="DH10B (phage-resistant)"
/note="Organ: testis; Vector: pcMv-SPORT6; Site_1: NotI;
Site_2: SalI: Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1
1 (bases 1 to 918)
NHH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
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                                                                                                                                          Length 1159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mark Maconochie, Ph.D. and Nancy
                                                                                                                                                                           Indels
                                                                                                                               Score 410.4; DB 14;
Pred. No. 6e-112;
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                                                                                                                                          tch 40.1%;
al Similarity 91.8%;
468; Conservative
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko Laboratory
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LiAMN1933 row: p column: 20
High quality sequence stop: 799.
Location/Qualifiers

1. 823
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I (bases 1 to 823)
II (bases 1 to 823)
INTH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for Rull-length clones and constructed by Life Technologies.
Note: this is a NH_MGC Library.
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/clone="IMAGE:5367043"
/clone_lib="NIH_MGC_94"
                                  BI738966.1 GI:15715979
                                                                                                                                                                                                               Unpublished (1999)
mRNA sequence.
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            ACCESSION
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Search completed: June 24, 2003, 10:54:14 Job time: 1468 secs

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/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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-08-614-877-1

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Maximum Match 100%
Listing first 45 summaries
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US-08-961-527-8 US-09-134-001C-1035 US-08-283-917-8 US-08-287-916-8 US-08-247-902A-1 US-08-247-902A-1 US-09-227-357-75 US-09-227-357-75 US-09-961-527-163 US-08-960-022-19 US-08-08-960-022-19 US-08-08-08-08-08-08-08-08-08-08-08-08-08-	ALIGNMENTS .	8576el e Famil 9,300A 208	Score 1023; DB Pred. No. 0; Mismatches	FFGCTGATGTTG 	raacaageteea 	rccagaaaacag 	CTGATGCTTTAG 	AGGCTCTCACCT
	ALIC	789300A ura A. . No. 645857 nt Enzyme F US/09/789,3 2-20 60/183,208 7	b; Sc b; Pr 0;	CATCTCCT	ACCAGTGC:	TGAACTCT	CTTGGTTCC 	CCATGGCC/
6211 1275 4 2085 2 2085 2 2085 2 1940 1 1910 1 1910 1 1910 2 3357 4 4651 2 4651 2 4651 2 4651 2 8351 4 3319 4 289 4		''ULT 1 Gg-789-300A-1 Gequence 1, Application US/09789300A Gatent No. 6458576 APPLICANT: Meyers, Rachel APPLICANT: Meyers, Rachel APPLICANT: Meyers, Rachel TITLE OF INVENTION: 22406, A No. 6458 TITLE OF INVENTION: Dependent Enzyme FILE REFERENCE: 35800/208926 CURRENT APPLICATION NUMBER: US 60/183; PRIOR FILING DATE: 2001-02-20 PRIOR PILING DATE: 2000-02-17 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastEED for Windows Version TYPP: DNA TYPP: DNA GRGANISM: HOMO SapienS FEATURE: NAMMEKEY: CDS LCCATION: (69)(1091)	100.0% larity 100.0% Conservative	CAGTATTG 	CACCTCAC 	TTCAAATG	CGTCAGAAG CGTCAGAAG	CAGTGGAAA CAGTGGAAA
		0A-1 645876 645876 645876 6758	Match Local Similarity Les 1023; Conser	ATGTGTGC ATGTGTGCC	SATTCTATO 	AATCTTTTO	CTCAATGC CTCAATGC	ACTCACAGO
3 4 4 8 8 8 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9		SULT 1 Sequence 1, Application Deatent No. 645876 GENERAL INFORMATION: APPLICANT: Meyers, Rach APPLICANT: Meyers, Rach APPLICANT: MIGOLPh-Owe TITLE OF INVENTION: De FILE REFRENCE: 3580/2 CURRENT APPLICATION NUMB FRICH FILING DATE: 2000 NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEO for W SEQ ID NO. LENGTH: 1770 LENGTH: 1	y Match Local S hes 1023	1 69	61 (121 2	181 (249 (309
24 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -		RESULT US-09- Seque Pate Pate APP TIT TIT CUR PRI PRI PRI SEO TY ORR TY	Query Ma Best Loc Matches	Qy Db	Qy Db	Qy Db	Qy Dp	Qy
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301 CCTGCTTATATTGTGGTGCCCCAGACAGCTCCAGACTGTAAAAAACTTGCAATACAAGCC 360

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ź			Db 4	Qy 4	Db 4	Oy 4	c qa	Qy 5	9 qa	0y .	9 qa	0у 6	Db 7	0y 7	Db 7	Qy 7	B qa		6 qa		6 qa	δу 9	Db 10	Qy 102	Db 10	RESULT 2 US-09-789-3 Sequence Patent No GENERAL I APPLICAN TITLE OF TITLE O	; PRIOR AP ; PRIOR FI	SOFTWARE	: LENGTH: 1020 ; TYPE: DNA	; ORGANISI

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                                            GATTCTATCGACCTCACACCAGTGCTAACAAGCTCCATTTTGAATCAACTAACAGGGCGC
                                                                           CCTGCTTATATTGTGGTGCCCCAGACAGCTCCAGACTGTAAAAAACTTGCAATACAAGCC
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     ery Match 99.7 st Local Similarity 100.7 tches 1020; Conservative
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1936 CGGTCGCCGGACTGCTGGAGCACC 1913

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APPLICANT: Rozman, Renee J.

TITLE OF INVENTION: Methods of Optimizing Substrate Pools and

TITLE OF INVENTION: Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval

TITLE OF INVENTION: in Bacteria and Plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   225 AGAACAGAAAGCGCACGCGTGATCACTGCTTCTGCGGGTAACCACGCGCACGGCGTCGC 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Gary M. Bond, Monsanto Company, A3SB ·800 No. 5942660th Lindbergh Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 5.6%; Score 57; DB 2; Best Local Similarity 43.6%; Pred. No. 1.9e-08; Matches 255; Conservative 0; Mismatches 330.
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                                                                                                                                                                                                                                                                                                          Clemente, Thomas E.
Connor-Ward, Dannette V.
Fedele, Mary J.
Fry, Joyce E.
                                                                       Sequence 1, Application US/08628039 Patent No. 5942660
                                                                                                                                                                                                                                       Padgette, Stephen R.
Stark, David M.
Hinchee, Maud A. W.
                                                                                                                                         Gruys, Kenneth J.
Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bond, Gary
                                                                                                                                                                                                                                                                                                                                                                                                          Howe, Arlene R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 1545 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (314)695-543 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
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STATE: Missouri
                                                                                                                 GENERAL INFORMATION:
APPLICANT: Gruys,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
                                                 US-08-628-039-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          509 TGCTGAACCAGGTTCCTTTGGTGGATGCACTGGTGGTACCTGTAGGTGGAGGAGGAATGC 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     569 TTGCTGGAATAGCAATTACAGTTAAGGCTCTGAAACCTAGTGTGAAGGTATATGCTGCTG 628
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                                                             GENERAL INFORMATION:
APPLICANT: Weber, J. Mark
APPLICANT: Luu, B. Minh
TITLE OF INVENTION: Method for Strain Improvement of
TITLE OF INVENTION: Erythromycin Producing Bacterium
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                ADDRESSEE: Rockey, Milnamow & Katz, Ltd.
STREET: 180 N: Stetson Avenue, 2 Prudential Plaza
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/153,599A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 62.4; DB 4;
Pred. No. 4.1e-10;
0; Mismatches 191;
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              Sequence 1, Application US/09153599A
Patent No. 6420177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V. REGISTRATION NUMBER: 38,978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: FEE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; MOLECULE TYPE: DNA (genomic) US-09-153-599A-1
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49.5%;
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LENGTH: 2299 base pairs
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EDNESS: single
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Best Local Similarity
Matches 190; Conserv
                                                                                                                                                                                                                                                                                                          STATE: Illinois
COUNTRY: U.S.A.
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US-09-153-599A-1/C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              336 CTGTAAAAAACTTGCAATACAAGCCTACGGAGCGTCAATTGTATACTGTGAACCTAGTGA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 CATCAAAGTCGACCGGCTGCGCGGCGTTCGGCGGCGAAGTGCTGCTCCACGGCGCGAACTT 404
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                                                                                                                                                                                                                                                                                                                    cch 5.6%; Score 57; DB 2; 31 Similarity 43.6%; Pred. No. 1.9e-08; 255; Conservative 0; Mismatches 330
                                              29,283
.mp. 38-21(13585)A
ATTORNEY/AGENT ....
NAME: BOND, Gary
REGISTRATION NUMBER: 29,283
REFERENCE/POCKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3412
// TELEPHONE: (314)695-3435
// INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TENGTH: 1545 base pairs
TENGTH: 1545 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
Padgette, Stephen R.
Stark, David M.
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Patent No. 5942660
GENERLI INFORMATION:
APPLICANT: GIUYS, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hinchee, Maud A. W.
                                                                                                                                                                                                                                                          ; MOLECULE TYPE: DNA (genomic) US-08-628-039-5
                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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Matches 25
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                                                                                                                                                 515
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             576 AATAGCAATTACAGTTAAGGCTCTGAAACCTAGTGTGAAGGTATATGCTGCTGAACCCTC
                                                                     TGAGTCCAGAGAAAATGTTGCAAAAAGAGTTACAGAAGAAACAGAAGGCATCATGGTACA
                                                                                                        TGATGAAGCGAAACGCAAAGCGATCGAACTGTCACAGCAGCAGGGGTTCACCTGGGTGCC
                                                                                                                                             TCCCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGGACAATTGCCCTGGAAGTGCTGAA
                                                                                                                                                                   525 GCAGGACGCCCATCTCGACCGCGTATTTGTGCCAGTCGGCGGCGGCGGCGTCTGCCTTG
                                                                                                                                                                                                                                                                                                                                    585 CGTGGCGGTGCTGATCAAACAACTGATGCCGCAAATCAAAGTGATCGCCGTAGAAGCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Gary M. Bond, Monsanto Company, A3. STREET: 800 No. 5942660th Lindbergh Boulevard CITY: St. Louis STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hinchee, Maud A. W.
Clemente, Thomas E.
Connor-Ward, Dannette V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
Padgette, Stephen R.
Stark, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08628039
Patent No. 5942660
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Fry, Joyce E.
Howe, Arlene R.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 13-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE
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APPLICANT:
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TITLE OF INVENTION: Methods of Optimizing Substrate Pools and TITLE OF INVENTION: Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval TITLE OF INVENTION: in Bacteria and Plants
NUMBER OF SEQUENCES: 11
      576 AATAGCAATTACAGTTAAGGCTCTGAAACCTAGTGTGAAGGTATATGCTGCTGAACCCTC 635
                                            585 CGTGGCGGTGCTGATCAAACAACTGATGCCGCAAATCAAAGTGATCGCCGTAGAAGCGGA 644
                                                                                                                                                                  696 TCCAGAAACCATAGCAGATGGTGTCAAATCCAGCATTGGCTTGAACACCCTGGCCTATTAT 755
                                                                                                                                                                                            105 AGGCTATITGCTGAAGGCGTAGCGCTAAAACGCATCGGTGACGAAACCTTCCGTTTATG 764
                                                                                                                          645 AGACTCCGCCTGCCTGAAAGCAGCGCTGGATGCGGGTCATCCGGTTGATCTGCCGCGCGT 704
                                                                                    636 AAATGCAGATGACTGCTACCAGTCCAAGCTGAAGGGGAAACTGATGCCCAATCTTTATCC
                                                                                                                                                                                                                                                   CAGGGACCTTGTGGATGATATCTTCACTGTCACAGAGGATGAAAT 800
                                                                                                                                                                                                                                                                          E: Gary M. Bond, Monsanto Company, A35B
800 No. 5942660th Lindbergh Boulevard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38-21(13585)A
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YSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemente, Thomas E.
Connor-Ward, Dannette
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08628039 Patent No. 5942660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Padgette, Stephen R.
Stark, David M.
Hinchee, Maud A. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bond, Gary
REGISTRATION NUMBER: 29,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION TELEPHONE: (314)694-3412
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gruys, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fedele, Mary J.
Fry, Joyce E.
Howe, Arlene R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bond, Garv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rozman, Renee J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1545 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (314)695-5435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (314)695-5435 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS: ADDRESSE: Gary M. E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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: Missouri
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US-08-628-039-8
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STATE:
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                                                             TITLE OF INVENTION: Methods of Optimizing Substrate Pools and TITLE OF INVENTION: Blosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalerd TITLE OF INVENTION: in Bacteria and Plants
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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43.6%; Pred. No. 1.9e-08;
tive 0; Mismatches 330; Indels
                                                                                                                                                                                                                         ADDRESSEE: Gary M. Bond, Monsanto Company, A3SB STREET: 800 No. 5942660th Lindbergh Boulevard
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38-21(13585)A
Clemente, Thomas E.
Connor-Ward, Dannette
Fedele, Mary J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 13-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: BOND, GATY
REGISTRATION NUMBER: 29,283
                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 38-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3412
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 43.6 Matches 255; Conservative
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                             CITY: St. Louis
STATE: Missouri
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                                                                                                                                                                                                                                                                                                                            63167
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Pred. No. 1.9e-08;
0; Mismatches 330; Indels
                                                                                                                PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                        38-21(13618)A
                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,388
FILING DATE: 13-MAR-1996
CLASSIFICATION: 800
                                                                                           PC-DOS/MS-DOS
                                                                                                                                                                            FILING DATE: 13-MAR-1996
CLASSIFICATION: 800
ATTORNEY/ACENT INFORMATION:
NAME: Cohen, Charles E.
REGIETRATION UNBRER: 34,565
REFERENCE/DOCKET NUMBER: 38-27
TELECOMMUNICATION INFORMATION:
                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBN PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-673-388-1
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Best Local Similarity 43.6%;
Matches 255; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                     1545 base pairs
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
                                                                                           OPERATING SYSTEM:
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STRANDEDNESS:
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                                                                                                                SOFTWARE:
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Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalera
in Bacteria and Plants
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                                                                                                                                                                          276 CTATGCTGCCAAATTGGAAGGAATTCCTGCTTATATTGTGGTGCCCCAGACAGCTCCAGA 335
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                                                                                                                                    284
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                                                                                                                                                                                                                                                                                                     345 CATCAAAGTCGACCGGCTGCGCGCTTCGGCGGCGAAGTGCTGCTCCACGGCGCGAACTT 404
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                                                                                                                      225 AGAACAGAAAGCGCACGGCGTGATCACTGCTTCTGCGGGTAACCACGCGCAGGGCGTCGC
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                                                   Gaps
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    Length 1545;
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Score 57; DB 2; Le
Pred. No. 1.9e-08;
0; Mismatches 330;
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Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
Padgette, Stephen R.
Stark, David M.
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  5.6%;
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                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: ME
TITLE OF INVENTION: BI
TITLE OF INVENTION: ir
NUMBER OF SEQUENCES: 1
                        Similarity
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APPLICANT: Gruys,
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Missouri
                                          255;
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Query Match
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TITLE OF INVENTION: Methods of Optimizing Substrate Pools and TITLE OF INVENTION: Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval TITLE OF INVENTION: in Bacteria and Plants
      515
                                                                                                                                                                      576 ANTAGCAATTACAGTTAAGGCTCTGAAACCTAGTGTGAAGGTATATGCTGCTGAACCTC 635
                                                                                                                                                                                                               585 CGTGGCGGTGCTGATCAAACAACTGATGCCGCAAATCAAAGTGATCGCCGTAGAAGCGGA 644
                                                                                                                                                                                                                                                     636 AAATGCAGATGACTGCTACCAGTCCAAGCTGAAGGGGAAACTGATGCCCAATCTTTATCC 695
                                                                                                                                                                                                                                                                                                                                                                              705 AGGGCTATITGCTGAAGGCGTAGCGGTAAAACGCATCGGTGACGAAACCTTCCGTTTATG 764
                                                                                                           645 AGACTCCGCCTGCCTGAAAGCAGCGCTGGATGCGGGTCATCCGGTTGATCTGCCGCGCGT
    456 TCCCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGGACAATTGCCCTGGAAGTGCTGAAA
                                             465 GCCGTTCGACCATCCGATGGTGATTGCCGGGCAAGGCACGCTGGCGCTGGAACTGCTCCA
                                                                                    696 TCCAGAAACCATAGCAGATGGTGTCAAATCCAGCATTGGCTTGAACACCTGGCCTATTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                               756 CAGGGACCTTGTGGATGATATCTTCACTGTCACAGAGGATGAAAT 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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Connor-Ward, Dannette V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/673,388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08673388 Patent No. 5958745 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Padgette, Stephen R.
Stark, David M.
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Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Clemente, Thomas E.
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TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,5
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Fry, Joyce E.
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Rozman, Renee J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1545 base pairs
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: Missouri
RY: USA
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Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalera
in Bacteria and Plants
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Pred. No. 1.9e-08;
0; Mismatches 330; Indels
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                                                                                                                                                                                                                                Clemente, Thomas E.
Connor-Ward, Dannette V.
Fedele, Mary J.
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APPLICATION NUMBER: US/08/673,388
FILING DATE: 13-MAR-1996
CLASSIFICATION: 800
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
               sequence 5, Application US/08673388
Patent No. 5958745
                                                                                                                                                                   Padgette, Stephen R.
Stark, David M.
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NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                            inchee, Maud A. W
                                                                                                     Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
                                                                                    Gruys, Kenneth J.
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Best Local Similarity 43.6%;
Matches 255; Conservative 0
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Howe, Arlene R.
Rozman, Renee J.
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INFORMATION FOR SEQ ID NO:
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STRANDEDNESS: double
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TITLE OF INVENTION:
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STATE: Missouri
COUNTRY: USA
                                                                GENERAL INFORMATION:
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US-08-673-388-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 1545;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 57; DB 2; Length 154 Pred. No. 1.9e-08; 0; Mismatches 330; Indels
                              BB4F
                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                          ADDRESSEE: Charles E. Cohen, Monsanto Company, STREET: 700 Chesterfield Parkway No. 5958745th
                                                                                                                                                                                                                                                                                                                                                                                                          38-21(13618)A
                                                                                                                                                                                                                                                                              US/08/673,388
                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         : Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6224
TELEFAX: (314)537-6047
                                                                                                                                                                                                                                                                                                                                                                                    34,565
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MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 5.6%;
Best Local Similarity 43.6%;
Matches 255; Conservative
                                                                                                                                                                                                                                                                                           13-MAR-1996
                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 1545 base pairs
                                                                                                                                                                                                                                                                                                                                                               NAME: Cohen, Charles E. REGISTRATION NUMBER: 34, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                   St. Louis
Missouri
                                                                                                                                                                                                                                                                                                  FILING DATE: 1
CLASSIFICATION:
                                                                                                              USA
                                                                                                                                  63198
                                                                                                                                                                                              COMPUTER:
                                             STREET:
CITY: St
STATE: M
COUNTRY:
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VENTION: Methods of Optimizing Substrate Pools and
VENTION: Methods of Optimizing Substrate Pools and
VENTION: Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalera
VENTION: in Bacteria and Plants
EQUENCES: 11
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                                                                                                                                                                                                                                                                                                                                     285 GTTTTCTTCTGCGCGGTTAGGCGTGAAGGCCCTGATCGTTATGCCAACCGCCACCGCCGA
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                                                                                                                             Length 1545;
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Pred. No. 1.9e-08; '
0; Mismatches 330;
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Clemente, Thomas E.
Connor-Ward, Dannette V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Padgette, Stephen R.
Stark, David M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
                                       ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-673-388-7
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Fry, Joyce E.
Howe, Arlene R.
                                                                                                                       Ouery Match
Best Local Similarity 43.69
Matches 255; Conservative
                       double
nucleic acid
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCES:
                     STRANDEDNESS:
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TITLE OF INVENTION: Methods of Optimizing Substrate Pools and TITLE OF INVENTION: Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval TITLE OF INVENTION: in Bacteria and Plants
                                  TGAGTCCAGAGAAAATGTTGCAAAAAGAGTTACAGAAGAAACAGAAGGCATCATGGTACA 455
                                                                                                                                                                                         576 AATAGCAATTACAGTTAAGGCTCTGAAACCTAGTGTGAAGGTATATGCTGCTGAACCCTC 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                          585 CGTGGCGGTGCTGATCAAACTGATGCCGCAAATCAAAGTGATCGCCGTAGAAGCGGA 644
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                                                                                       405 TGATGAAGCGAAACGCAAAGCGATCGAACTGTCACAGCAGCAGGGGTTCACCTGGGTGCC 464
                                                                                                                                                                                                                                                                                                                                   525 GCAGGACGCCCATCTCGACCGCGTATTTGTGCCAGTCGGCGGCGGCGGTCTGGCTGCTTG 584
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                                                                                                                                                      456 TCCCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGGACAATTGCCCTGGAAGTGCTGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               756 CAGGGACCTTGTGGATGATATCTTCACTGTCACAGAGGATGAAAT 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Charles E. Cohen, Monsanto Company, 700 Chesterfield Parkway No. 5959179th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TORNEX/AGENA TOTALES E. NAME: Cohen, Charles E. REGISTRATION NUMBER: 34,565
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Clemente, Thomas E.
Connor-Ward, Dannette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/08614877; Patent No. 5959179; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Padgette, Stephen R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eloppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gruys, Kenneth J.
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Fry, Joyce E.
Howe, Arlene R.
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N: 800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stark, David M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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STATE: .Missouri
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US-08-614-877-5
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Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalera
in Bacteria and Plants
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Indels
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Charles E. Cohen, Monsanto Company,
STREET: 700 Chesterfield Parkway No. 5959179th
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CUBRENT APPLICATION NUMBER: US/08/614,877
FILING DATE: 13-MRR-1996
CLASSIPICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Cohen, Charles E.
REGISTRATION NUMBER: 34,565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Connor-Ward, Dannette V.
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ZIP: .61198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
                                                                                                                                                                               Sequence 1, Application US/08614877
Patent No. 5959179
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Stark, David M.
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                                                                                                                                                                                                                                                                 Gruys, Kenneth J.
Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
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TELECOMMUNICATION INFORMATION:
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Fry, Joyce E.
Howe, Arlene R.
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TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 1545 base pairs
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TITLE OF INVENTION: Met)
TITLE OF INVENTION: BION
TITLE OF INVENTION: IN IN
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STRANDEDNESS: double
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Missouri
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Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyval in Bacteria and Plants
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                         Methods of Optimizing Substrate Pools and
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                                                                             NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles E. Cohen, Monsanto Company,
STREET: 700 Chesterfield Parkway No. 5959179th
                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
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Pred. No. 1.9e-08;
0; Mismatches 330,
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                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION:
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US-08-614-877-7
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ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1545 base pairs
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APPLICATION NUMBER: US,
FILING DATE: 13-MAR-19
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                      TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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Missouri
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                                                                                                                                                                CITY: STATE:
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Best Local
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Matches
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0; Mismatches 330;
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Patent No. 5959179
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Stark, David M.
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Kishore, Ganesh M.
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TELEPHONE: (314)537-6224 TELEPAK: (314)537-6047 INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
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Fry, Joyce E.
Howe, Arlene R.
                                                                             1545 base pairs
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Best Local Similarity 43.6
Matches 255; Conservative
                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
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    285 GITITCITCIGCGCGGTTAGGCGTGAAGGCCCTGATCGTTATGCCAACCGCCACCGCCGA 344
                                                                    396 TGAGTCCAGAGAAAATGTTGCAAAAAGAGTTACAGAAGAAACAGAAGGCATCATGGTACA 455
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Biosynthesis of Poly-B-hydroxybutyrate-co-poly-B-hydroxyvalera
in Bacteria and Plants
11
TCCAGAAACCATAGCAGATGGTGCAAATCCAGCATTGGCTTGAACACCTGGCCTATTAT 755
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,877
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Pred. No. 1.9e-08;
0; Mismatches 330;
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Connor-Ward, Dannette V.
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Patent No. 5959179
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Stark, David M.
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Mitsky, Timothy A.
Kishore, Ganesh M.
Slater, Steven C.
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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Fry, Joyce E.
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ATTORNEY/AGENT INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ROZMAN, RITLLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
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US-09-889-609B-1 1018

1 atgtgtgctcagtactgcat......taccagacggtctgtttaa 1018 Title: Perfect score: Sequence:

IDENTITY_NUC Gaport 1.0 Scoring table:

2054640 seqs, 14551402878 residues Searched:

4109280 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

GenEmbl:* Database :

gb_ro:* gb_sts: gb_sy:* gb_om:,

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em_ro:* em_pl:* em_pat:

em_htg_hum:* em_un:* em_vi:*

em_htg_other em_htg_mus:* em_htg_pln: em_htg_rod:

em_htgo_mus:*
em_htgo_other:* em_sy:* em_htgo_hum:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Mus m	mRNA linear ROD 18-NOV-1999 NA, complete cds. raniata; Vertebrata; Euteleostomi; ciurognathi; Muridae; Murinae; Mus. nyder,S.H. synthesizing D-serine to regulate neurotransmission
ID	0 AF148321 0 BC011164 AY024420 AY024420 AY024420 AX224418 AX224418 AX224418 AX224418 AX2243169 AX229575 AX229575 AX229575 AX229575 AX229575 AX229575 AX22030 AX229575 AX22031531 AC011909 AC0117499 AC0117499 AC0117499 AC0117499 AC0117499 AC0117499 AC0117499 AC0117499 AC0117499 AC0117499 AC01189 AC0117499 AC0117499 AC0117499 AC0117499 AC0117499 AC01189 A	1197 bp cemase mR cordata; C dentia; S dentia; S al enzyme
% Query Match Length DB	99.3 99.3 1197 99.4 1110 99.4 1110 99.4 1110 99.5 99.6 99.3 1110 99.6 1110 99.6 1110 99.6 1110 99.6 1110 99.6 1110 99.6 1110 99.6 1110 99.6	8321 musculus serin 8321.1 GI:644 musculus. ryota; Metazoa alia; Eutheria alia; Eutheria sker, H., Black ne racemase: a
Result No. Score		AF148321 LOCUS AF148321 LOCUS ACCESSION VERSION AF14 VERYWORDS SOURCE ORGANISM MUS ORGANISM MUS AUTHORS MOIO TITLE Seri

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BC011164 1411 bp mRNA linear ROD 07-AUG-2002 Mus musculus, Similar to serine racemase, clone MGC:18670 IMAGE:4195695, mRNA, complete cds.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7305520.
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Sciurognathi; Muridae; Murinae; Mus
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Martin, R.G., Muzny, D.M.,
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Submitted (25-UUL-2001) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                    961 TCCCTGAACTGGGTGGGCAGGCTGAACGGCCAGCTCCTTACCAGACGGTCTGTTT 1016
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                                 ACTGTCACCGAAGATGAAATCAAGTATGCAACCCAGCTGGTGTGGGGGGAGAATGAAACTG
                AAACCTAGTGTGAAGGTATACGCTGCTGAGCCCTCGAATGCAGATGACTGCTACCAGTCT
                                                                                AAACTGAAAGGAGAACTGACCCCCCAATCTTCATCCTCCAGAAACCATAGCAGATGGTGTC
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
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Yoon, V.S., Kowis, C.R., Lawrence,
Richards, S., Gibbs, R.A.
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/db_xref="taxon:10090"
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Mammalia; Eutheria; Rodentia;
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KCELFQXTGSFKIRGALNAIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPA
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AGGGTIALEVLNQVPLVDALVVPVGGGWAGITAITIRALEKSYKVYAAEPSNADCY
QSKLKGELTPNLHPPETIALOKSSIGIATWI IRDLVDDVFTVTEDEIKYATQLVWG
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Natl. Acad. Sci. U.S.A. 96 (23), 13409-13414 (1999)
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                                                                            Direct Submission
Submitted (03-MAY-1999) Neuroscience,
North Wolfe St., WBSB 806, Baltimore,
Location/Qualifiers
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                                                                                                                                                                                                                                                                     /product="serine racemase"
/protein_id="AAF08701.1"
/db_xref="G1:6448865"
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/db_xref="taxon:10090"
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Wolosker, H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 2.1e-211;
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A human pyridoxal-phosphate dependent
therefor
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Millennium Pharmaceuticals, Inc. (US)
Location/Qualifiers
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/db_xref="taxon:9606"
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                                                                                                                       /translation="MOAQYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFF
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RMKLLIEPTAGVALAAVLSQHFQTVSPEVKNVCIVLSGGNVDLTSLNWVGQAERPAPY
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                      month
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Pred. No. 1.9e-267;
0; Mismatches 3; In
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                                                                                        /product="Similar to serine
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/db_xref="GI:15029881"
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                                                        /note="Vector: pCMV-SPORT6"
288. .1307
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                                                                                /codon_start=1
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/translation="MCAQYCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFF
KCELFQKTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPA
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RMKLLIEPTAGVGVAAVLSQHFQTVSPEVKNICIVLSGGNVDLTSSITWVKQAERPAS
YQSVSV,"
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Pred. No. 2.1e-211;
0; Mismatches 122;
                  racemase"
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Best Local Similarity 87.7%;
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              GTCTCTCCAGAAGTAAAGAACGTCTGCATTGTACTCAGTGGGGGGAATGTAGACCTAA--
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                                                 AGAATTATGCAAGAAACAGAAGGCATCTTGGTCCATCCCAACCAGGAGCCTGCAGTGATA
                                                                                                   GCTGGACAAGGAACAATTGCCCTGGAAGTGCTGAACCAGGTTCCCTTGGTAGATGCACTG
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Xia,M., Liu,Y. and Connolly,T.M.
Direct Submission
Submitted (08-MAY-2001) Pharmacology,
West Point, PA 19486, USA
Location/Qualifiers
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mRNA,
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/db.xrefe"taxon:9606"
/chromosome="17"
/map="17p13"
1. .1023
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Xia,M. Liu,Y. and Connolly,T.M. Molecular cloning and expression human NT2N cells
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Mammalia; Eutheria; Primates;
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VERSION
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AUTHORS
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-	841 CTCATTGAGCCGACTGCTGCGCTGCAGTGCTGCTGTCTCCAGCATTTCCAAACA	Db 841 CTCATTGAACCTACAGCTGGTGTTGGAGTGGCTGCTGTCTCAACATTTTCAAACT 900 Qy 901 GTCTCTCCAGAAGTAAAGAACGTCTGCATTGTACTCAGTGGGGGGAATGTAGACCTAA 958	901 GTTCCCCAGAAGTAAAGAACATTCTATTGTGCTCAGTGGTGGAAATGTAGACTTAACC 96	DD 951 TCTCCATAACTIGGGTGAAGCCTGAAAGCCCAGCTCTTACCAAGCGCTTT 1010 DD 961 TCCTCCATAACTIGGGTGAAGCCTGAAAGGCCAGCTTCTTATCAGTCTGTTTCTGT 1019	AF169974 AF169974 1166 bp mRNA linear PRI 27-OCT-2000 DEFINITION Homo Sapiens serine racemase mRNA, complete cds.	VERSION AF169574 VERSION AF169574.1 GI:11034784 KEYWORDS . MOMO Sapiens.		acemase: moleular cloning, lysis , 183-188 (2000)		AL		/ub_xreif="taxon:9000" /tissue_type="brain" 171039 /function="catalyzes L- to D-serine racemization"	/coduct="gerine racemase" /product="gerine racemase" /protein_id="AAG27081.1" /db_xref="GI:11034785" /translation="workyres"	CLEPORTGER IN THE TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TOTAL TO THE TOTAL	MAKLLEFTAGVGVAAVLSQHFQTVSPEVKNICIVLSGGNVDLTSSITWVKQAERPAS YQSVGSW 333 a 238 c 275 g 320 t ORIGIN	Query Match Best Local Similarity 87.7%; Pred. No. 2.1e-211; Matches 894; Conservative 0; Mismatches 122; Indels 3; Gaps 1;	Qy 1 ATGTGTGCTCAGTACTGCTTTGCTGAAAAAGCTCATATCAACATTCAA 60	OY 61 GACTCTATCCACCTCACCCCAGTGCTAACAAGCTCCATTTTGAATCAAATAGCAGGGCGC 120	Qy 121 AATCTTTCTTCAAATGTGAGCTCTTCCAGAAAACTGGGTCTTTTAAGATTCGAGGTGCC 180

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Unpublished

2 (bases 1 to 2477)

Is Isogal, T. and Outsuki, T.

Direct Submission

Submitted (23.40G-2000) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

(E-mail:genomicsehri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Blotechnology; CDNA library construction, 5'- & 3'-end one pass sequencing and clone selection:
Helix Research Institute (supported by Japan Key Technology Center etc.) and Departement of Virology, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                 AKU23169

2477 bp mRNA linear PRI 01-AUG-2002 Homo sapiens cDNA FLJ13107 fis, clone NT2RP3002501, weakly similar to THREONINE DEHYDRATASE CATABOLIC (EC 4.2.1.16).
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nishikawa, T., Naqai, K., Sugano, S., Shiratori, A., Sudo, H., Wagatsuma, M., Hosoiri, T., Kaku, Y., Kodaira, H., Kondo, H., Sugawara, M., Takahashi, M., Chiba, Y., Ishida, S., Murakawa, K., Ono, Y., Takiguchi, S., Watanabe, S., Kimura, K., Murakami, K., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nagahari, K., Masuho, Y., Ninomiya, K. and Iwayanagi, T. NEDO human cDNA sequencing project
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   AAGCTGAAGGGGAAACTGATGCCCAATCTTTATCCTCCAGAAACCATAGCAGATGGTGTC
                                                                                                                                                                                           AAATCCAGCATTGGCTTGAATACCTGGCCTATTATAAGAGACCTTGTGGATGATGTCTTC
                                                     oligo capping; fis (full insert sequence).
Homo sapiens teratocarcinoma cell_line:NT2 cDNA to mRNA,
clone_lib:NT2RP3 clone:NT2RP3002501.
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AGQCTIALENLAVPEVDALVVPVGGGGMLACIAITVKALKPSVKVYAAEPSKADDCY
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human pyridoxal-phosphate dependent
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Catarrhini; Hominidae; Homo.
                                               1 ATGTGTGCTCAGTACTGCATCTCCTTTGCTGATGTTGAAAAAGCTCATATCAACATTCAA
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.7e-211;
                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 5.7e-211;
0; Mismatches 123;
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Regulation of human serine racemase Patent: WO 0173077-A 1 04-OCT-2001;
Bayer Aktiengesellschaft (DE)
                                                                                                                                                                                                                                                                                                                                                                                                       Score 806.2;
Pred. No. 5.7e
                                                                                                                                                                                                                                                                                                                                                                       362
                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
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268 c 319 g 36:36
                                                                                                                                                              1336 bp
Patent WO0173077
                                                                                                                                                                                                                                             Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                       ch 79.2%;
11 Similarity 87.6%;
893; Conservative
                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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AUTHORS
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                                                                                                                                                              Gaps
                                                                                                                                                              3;
                                                                                                                                       2477;
                                                                                                                                       Length
                                                                                                                                                              Indels
                                                                                                                                     Score 807.8; DB 9;
Pred. No. 1.9e-211;
0; Mismatches 122;
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                                                                                                                                      79.48;
87.78;
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                                                                                                                                     Query Match 79.4
Best Local Similarity 87.7
Matches 894; Conservative
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TQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVKNICIVLSGGNVDLTSSITWVKQ
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                   /note="similarity to serine racemase (Mus
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Pred. No. 5.5e-172;
); Mismatches 114;
                                                     protein"
                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                          629
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                                                                                                                                                                                                      /gene="DKFZp762A2415"
2253
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                                       /codon_start=1
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86.4%;
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This clone (DKF2P762A2415) is available at the RZDD in Berlin.
Please contact the RZDD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY: Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://mips.gsf.de/proj/cDNA/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSM805450 2264 bp mRNA linear PRI 12-JUL-2002 Homo sapiens mRNA; cDNA DKFZp762A2415 (from clone DKFZp762A2415). ALB34378.1 GI:21740048
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                  GTGGTACCAGTAGGAGGAGGAGGAGGTTGCTGGAATAGCCATTACAATTAAGGCCCTG
                                                                 GTGGTACCTGTAGGTGGAGGAATGCTTGCTGGAATAGCAATTACAGTTCAGGCTCTG
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                                                                                                                                                                      AAACTGAAAGGAGAACTGACCCCCAATCTTCATCCTCCAGAAACCATAGCAGATGGTGTC
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Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Car
Research Center (DRE2); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="bkR2p762A215"
/tissue_type="melanoma (MeWo cell line)"
/clone=lib="762 (synonym: hmel2). Vector pSportl; DH10B; sites NotI + SalI"
/dev_stage="adult"
/close_lib="762 (synonym: hmel2). Vector pSportl; lower stage="adult"
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/gene="DKF2p762A2415"
<1. .867
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HSM805450
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TITLE
JOURNAL
COMMENT
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VERSION
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αn	/21 GIGCIGICTCAACATTTTCAAACTGTTTTCCCCAGAAGTAAAGAACATTTGTATTGTGCTC 780	 Db	
Οy	937 AGTGGGGGGAATGTAGACCTAACCTCCCTGAACTGGGGGGCAGGCTGAACGGCA 993	713	
Dp	781 AGTGGTGGAAATGTAGACTTAACCTCCTCCATAACTTGGGTGAAGCAGGCTGAAAGGCCA 840	125650	
Oy Dp	994 GCTCCTTACCAGACGGTCTGTTT 1016 	773	
RESULT 10 AL604066/C		803	
LOCUS	AL604066 : 184151 bp DNA linear ROD 14-MAR-2002 ON Monse DNA sequence from clone RD23-174M12 on chromosome 11	Db 125530 CTGAC	125530 CTGACAGTAGATCACATACTTATCACAACAAACCCAAATGTCTACTTCATTTTTCGAATG 125471
ACFECTION	complete s	Qy 803	803
VERSION KEYWORDS		Db 125470 TAACC	125470 TAACCTACTAGACTCCGGCTCCGTTTCTTGTTTCATTAACCCTTGCTCCTTTCTGTGCCA 125411
SOURCE ORGANISM	house mouse. SM Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Qy 803AGT Db 125410 ACAGT	803AGTATGCAACCCAGCTGGTGGGGGAGAATGAAACTGCTCATTGAGCCGACTGCTGG 860
REFERENCE		Qy 861 CGTGG	CGTGGCACTGGCTGCTGTCTCAGCATTTCCAAACAGTCTCTCCAGAAGTAAAGAA 920
AUTHORS TITLE		 125350 CGTGG	
	Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk	Qy 921 CGTCT	CGTCTGCATTGTACTCAGTGGGGGAATGTAGACCTAACCTCCCTGAACTGGGTGGG
COMMENT	On Mar 21, 2002 this sequence version replaced gi:17902958. During sequence assembly data is compared from overlapping clones.	Db 125290 cGrcr	CGTCTGCATTGTACTCAGTGGGGGGAATGTAGACCTAACCTCCCTGAACTGGGTGGG
	Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the	Qy 981 GGCTG	GGCTGAACGGCCAGCTCCTTACCAGACGACTGTTT 1016
	variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with	Db 125230 GGCTG	125230 GGTGAACGGCCAGCTCCTTACCAGACGGTTTCTGT 125195
	only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all	RESULT 11	
	regions were cities doubte strained of sequenced with an afternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems each	LOCUS AC044847	205910 bp DNA linear
	as compressions and repeats; all regions were covered by at least		unordered pieces.
	one plasmid succione or more than one Mis succione; and the assembly was confirmed by restriction digest. The following	z	7.3 GI:11597106
	ableviations are used to associate primary accession numbers given in the feature table with their source databases: Em., EMBL; Sw., SWISCRPOW. Tr. TREMEL: Wr. WADDEDE: Information on the modules	SOURCE MUS MUS MUS	HTG; HTGS_PHASEI; HTGS_DRAFT. MNS muscalus.
	database can be found at		mus musculus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
	inch://www.sauyer.ac.uk/Frojects/C_eregans/wormpep KF23-1/4M1/ is from the RPCI-23 Mouse PAC Library	REFERENCE 1 (bas	malia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 205910)
	Constructed by the group of Fieler de Jong. For further details see http://www.chori.org/bacpac/home.htm VFCTOR: DRAFG? 6		Birren, B., Lincon, L., Nusbaum, C. and Lander, E. Mus musculus chromosome 11, clone RP23-5305
	This sequence is the entire insert of clone RP23-174M12 The true right and of clone RP33-194D5 is at 82810 in this sequence	REFERENCE 2 (bases 1	Siled es 1 to 205910)
FEATURES	tage of croic arts 1945 to croto in this sequence. ES Location/Qualifiers Onrea 1 184151	AUINONS BILLEN, Anderso	b., Lintou, L., Nusbaum, C., Lander, E., Abfandmi, H., Allen, N., In.S., Baldwin, J., Barna, N., Bastien, V., Beda, F., H., Foruthanland Process of Proces
;)		Collymo	VALY, L., Boundgalet, D., Blown, A., Burkel, V., and Ano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., re a Cooke D Dataslanck News K Miss 1 S
	/chromosome="11" /clone="RP23-174M12"	Dodge, S Galadan	. Downto, W. Doyle, M. Ferreira, P. FitzHugh, W. Gage, D. J. Cardyna, S. Ginde, S. Groette M. Graham, W.
BASE COUNT	46879 a	Grand-F Howland	ierre, V. Grant, G., Hagos, B., Heaford, A., Honton, L., I. Tibor, T. Johnson R. Innes C. Kann, I. Kantas, A.
ORIGIN		Klein, J Levine,	. LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
Query Match Best Local	25.3%; Score 257.2; DB 10; Length 184151; Similarity 73.1%; Pred No. 6.1e-60;	McCarth	McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,
	**** COURSELVALIVE U, MISHIACCHES 3; INDEES 132; GAPS	Murpny, O'Neil,	T., NAYLOL,J., NOTMAN,C.H., O'CONNOL,T., O'DONNELL,P., D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N.,
Oy Ph	593 AGGCCCTGAAACCTAGTGTGAAGGTATACGCTGCTGAGCCTCGAATGCAGTGACTGCT 652 	Pisani, Roy, A.,	C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Santos, R., Schauer, S., Severy, P., Spencer, B.,
		Stange- Tesfaye	Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
Š		VASSILI	ev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,w.J.,

TITLE JOURNAL

COMMENT

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oof 100 bp
contig of 12282 bp in length
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contig of 14419 bp in length
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Location/Qualifiers
                                                                                                                                                                                                                                                             10: gap of 100 bp 73.50: contig of 6140 bp in length 550: gap of 100 bp 82345: contig of 9095 bp in length
                     in length
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                                                                                                                                                                                                o of 100 bp contig of 4678 bp in length
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5981 bp in length
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                                                                 p of 100 bp
contig of 4611 bp
   34: gap of 100 bp
34444: contig of 3310 bp
                                                                                               43728: gap of 100 bp 47588: contig of 3860 bp
                                                                                                                                 88: gap of 100 bp 52019: contig of 4331 bp
                                                                                                                                                                 oof 100 bp
contig of 3932 bp
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83. .1117
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66910: contig of
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chromosome="11"
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94727: cont
                       38917: ~*
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                          Submitted (12-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Dec 7, 2000 this sequence version replaced g1:10954406.
                                                                                                                             ...... Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will. be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 consists of 37 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently
                                                                                          Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                      Sequencing vector: Plasmid; n/a; 96% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
                                                                                                                                                                           Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 3.8 in Q20 bases; agarose-fp
Quality coverage: 4.2 in Q20 base.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 bp
of 1222 bp in length
100 bp
of 1463 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100 bp of 1698 pp in length 100 bp of 1060 bp in length
                                                                                                                                                                                                                                                                                                                                   Consensus quality: 18882 bases at least 040 Consensus quality: 197278 bases at least 030 Consensus quality: 200395 bases at least 020
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1560 bp in length
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1073 bp in length
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contig of 1515 bp in length
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2610 bp in length
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f 898 bp in length
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contig of 635 bp in length
                                                                             All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
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Coung, G., Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                      Insert size: 220000; agarose-fp
Insert size: 202310; sum-of-contigs
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12705: cont
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483 1117: cc
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FPLNPRVIKSOKKPNMAMEVCYTDAAADMEEDLKVLMKADPDHQESLOTEAIPDPMEG
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EGFMEEESQDGSGEEEEEECETMTLGESVRDDLYDEKVDEEDEERMLEKYKQERLEEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 36 Row: m Column: 16 Paises IRAK Plate: 18 Row: m Column: 16 Paised for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MAKVADTILFLLDPLEGWDSTGDYCLSCLFAQGLPTYTLAVQGL
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RTFPPASVLLFKQRRNGMHSLIATGHLFSVDPDRMVIKRVVLSGHPFKIFTKMAVVRY
MFFNRGCDVV"
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                                              Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M., Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.
                                                                                                                                      Direct Submission
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MCC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
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MMTV-LTR/Wntl model. Expression driven by an NMTV-LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         593 AGGCCCTGAAACCTAGTGTGAAGGTATACGCTGCTGAGCCCTCGAATGCAGATGACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="Similar to hypothetical protein FLJ10534"
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                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Glibert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing, Psylor College of Medicine Human Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pcMV-SPORT6"
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Mammalia; Eutheria; Rodentia;
1 (bases 1 to 3379)
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                          Mus musculus
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ORIGIN
                        ORGANISM
                                                                                                                AUTHORS
TITLE
JOURNAL
                                                                                          REFERENCE
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BC031531.1 GI:21619397
MGC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 205910;
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KEYWORDS
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<pre>Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Morgan,M., Morris,S.,</pre>	Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oradov, Parc, Parton, B., Perry, J., Perez, L., Daten, P., Parc, P., Parton, B., Perez, J., Perez, L.,	Fereis, L., Fitchens, R., Filmus, E., Fuller, Willes, W., Ren, I., Rolles, R., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H.,	Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S.,	Usmanı, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q., Wang, S., Ward Moore, S., Warren, R., Washington, C., Watlington, S.,	WILLIAMS, C., WILLIAMSON, A., WLECZYK, K., WOOGEN, S., WOFIEY, K., WU, Y., WU, Y., WU, Y., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.	neinscook, or and others. Direct Submission . Innertished	E 2 (bases 1 to 101814) S Worley K.C.		S Worley K.C. Direct submission Direct submission Submitted (23-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One		Center: Baylor College of Medicine Center code: BCM	Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc.help@bcm.tmc.edu 	Center project name: GWZI Center clone name: CH230-280H23		Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 43731 bases at least 040	Consensus quality: 47905 bases at least Q30 Consensus quality: 51501 bases at least Q20	* NOTE: Estimated insert size may differ from sequence length	<pre>" (see incl')/***'.igsc.iom:.mc.edu/uccs/ceinank_dratt_data * NOTE: This is a 'working draft' sequence. It currently * consists of 61 contins</pre>	* is not known and their order in this sequence record is	* runs of N, but the exact sizes of the gaps are unknown.	* ints fecord will be updated with the inished sequence * as soon as it is available and the accession number will * to accession.	preserved. 1 1045: contig of 1045	2200: contig of 1055	2300: gap of unknown 3345: contig of 1045	 3445: gap of unknown 4445: contig of 1000 	4545: gap of unknown 5575: contig of 1030	5675: gap of unknown 6696: contig of 1021	5/96: gap of unknown 7807: contig of 1011	* 7808 7907: gap of unknown length * 7908 8910: contig of 1003 bp in length * 8911 9010: gap of unknown length
		•			:	TITLE	REFERENCE AUTHORS	JOURNAL	AUTHORS TITLE JOURNAL	COMMENT																			
3163 ACCAGTCTAAACTGAAAGGAGAACTGACCCCCAATCTTCATCCTCCAGAAACCATAGCAG	VY /13 ATGGTGTCACATTGGCTTGAATACTGGCCTATTATAAAGAGACCTTGTGGATG 772 	Qy 773 ATGTCTTCACTGTCACGAAGATGAAATCA	Qy 803 802	Db 2983 CTGACAGTAGATCACATACTTATCACAACAAACCCAAATGTCTACCTCATTTTTCGAATG 2924	Оу 803 802 .	Db 2923 TAACCTACTAGACTCCGGCTCCGTTTCTTGGTTCATTAACCCTTGCTCCTTTCTGTGCCA 2864	QY 803AGTATGCAACCCAGCTGGTGGGGGAGAATGAAACTGCTCATTGAGCCGACTGCTGG 860 11 11 11 11 11 11 11 11		QY 921 CGTCTGCATTGTACTCAGTGGGGGAATGTAGACCTAACCTCCCTGAACTGGGTGGG	Qy 981 GGCTGAACGGCCAGCTCCTTACCAGACGGTCTGTT 1016	Db 2683 GGCTGAACGCCCAGCTCCTTACCAGGTTTCTGT 2648	RESULT 13 AC122087/c	LOCUS AC122087 101814 bp DNA linear HTG 23-JUL-2002 DEFINITION RATUS norvegicus clone CH230-280H23, *** SEQUENCING IN PROGRESS *** fl unordered nienes	AC122087		ORGANISM Rattus norvegicus Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodeniia, Sciuroanathi, Muridae, Murinae.	REFERENCE 1 (bases 1 to 101814)	AUTHORS Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Avele, M. Banks, T.	Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bonrie, J. Bong, C. Briggs, M. Brons, M	Buhay,C., Darton,P., Burkett,C., Burnell,K.L., Byrd,N.C., Carron W. F. Carton M. Carron C. E. Charles T. Charles	Chen, G., Chen, R., Chen, Z., Chowdhy, I., Christopoulos, C., Cleveland, C., Crow, C., M. P., Phorne S. D. Pavid B.	Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, B., Delanev, K. P., Delanev, D. Den B. I. Ding V. Dink U. B.	Douthwaite, K.J., Draper, P. Dugan-Rocha, S., Durbin, K.J.,	<pre>Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P.,</pre>	Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,	<pre>hariis,C., hariis,K., hart,M., havlak,P., hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C., Hollins,B.,</pre>	Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jackson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,	Kratovic,J., Kureshi,A., Landry,N.; Leal,B., Lewis,L., **Lear T. C., Lewis,L., **Lewis,L., Lear Lewis,L., Lewis,L., **Lewis,L., Lewis,L., Lewis,L., Lewis,L., **Lewis,L., Lewis,L., Lewis,	Lozado, L.

tilg of 127/ bp 120 of unknown leng tilg of 1023 bp 10 of unknown leng tilg of 1751 bp 10 of unknown leng tilg of 1453 bp 10 of unknown leng tilg of 1013 bp 10 of unknown leng tilg of 1012 bp 10 of unknown leng tilg of 1013 bp 10 of unknown leng tilg unknown leng tilg of 1013 bp 10 of unknown leng tilg unkno	of unknown length titig of 1491 bp in length titig of 1012 bp in length of unknown length length of 1370 bp in length of 1370 bp in length of 1023 bp in length of 1245 bp in length of 1245 bp in length of 1000 bp in length of unknown length titig of 1364 bp in length of 1427 bp in length of 14268 bp in len	of unknown length hery of unknown length hery of unknown length hits of 1006 bp in leng this of 1006 bp in leng of unknown length hits of 1491 bp in leng to of unknown length hits of 1524 bp in leng of 1677 bp in leng of unknown length hits of 1677 bp in leng of unknown length hits of 1677 bp in leng of unknown length hits of 2415 bp in leng of unknown length hits of unknown length length hits of unknown length hits of unknown length length hits of unknown length le	titig of 1599 bp to g unknown len to of unknown len titig of 1972 bp titig of 1972 bp titig of 1332 bp titig of 1332 bp titig of 1332 bp titig of 1074 bp of unknown len titig of 1074 bp of unknown len titig of 1074 bp to of unknown len titig of 1427 bp to of unknown len titig of 1433 bp titig of 1433 bp titig of unknown len titig of unknown len titig of unknown len titig of unknown len titig of unknown len
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0000 0000 0000 0000 0000 0000 0000 0000 0000	1965/3 1965/3 1967/3 201106 20	44946 61107	7864666666676677 776666666666667

95368 ATGCCGTCAAGTCCAGCATTGCCTTAAATACCTGGCCTATTATAAGGGACCTTGTGGACG 95309 95248 TAACTTCCCAGGCACTGACAGACCATTCCCTTAACCTGTGGGAAATGGTAGCTCACCTAC 95189 PRI 11-DEC-2001 complete cds. 802 811 ATGGTGTCAAATCCAGCATTGGCTTGAATACCTGGCCTATTATAAGAGACCTTGTGGATG 772 812 CCCAGCTGGTGTGGGGGAGAATGAAACTGCTCATTGAGCCGACTGCTGGCGTGGCACTGG 871 991 653 ACCAGTCTAAACTGAAAGGAGAACTGACCCCCAATCTTCATCCTCCAGAAACCATAGCAG -----AGTATGCAA 593 AGGCCCTGAAACCTAGTGTGAAGGTATACGCTGCTGAGCCCTCGAATGCAGATGACTGCT Score 212.2; DB 2; Length 101814; Pred. No. 1.6e-47; 0; Mismatches 38; Indels 141; Gaps 3807 bp mRNA linear Homo sapiens, clone MGC:29514 IMAGE:4896567, mRNA, BC019090 GI:17512217 MGC f unknown length g of 1567 bp in length f unknown length g of 2543 bp in length in length in length bp in length in length length in length in length bp in l length length length length length length length length unknown of 1818 unknown of 2776 unknown of 1723 unknown unknown of 1725 of 1358 unknown 94948 CGCTCCTTAACAGACTGTTTCTGT 94924 992 CAGCTCCTTACCAGACGGTCTGTTT 1016 ot gap of contig gap of contig gap of gap of contig gap of contig gap of contig contig gap of contig 20.8%; 68.3%; 70388: 70488: 73311: 83470: 74459:74559: 76284 Conservative Homo sapiens. Homo sapiens Query Match Best Local Similarity Matches 386; Conser 65094 65194 67013 67113 68471 70389 70489 74460 74560 76285 76385 79161 79261 80828 713 773 803 803 RESULT 14
BC01909/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM ōλ g δy qq ò g ò qq ö g Ω Db ōλ qq δ q δ qq οy qq

PRI 29-SEP-2000

817

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3231 ATGGTGTCAAATCCAGCATTGGCTTGAACACCTGGCCTATTATCAGGGACCTTGTGGATG 3172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center: Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (sites)
Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Tashiro,H.,
Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T.,
Nakamura,Y., Isogai,T. and Sugano,S.
NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATGGTGTCAAATCCAGCATTGGCTTGAATACCTGGCCTATTATAAGAGACCTTGTGGATG 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                        oligo capping; fis (full insert sequence).
Homo sapiens signet ring cell carcinoma cell_line:KATO III cDNA mRNA, clone_lib:KAT clone:KAT06132.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 4140)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
Direct Submission
                                     713 ATGGTGTCAAATCCAGCATTGGCTTGAATACCTGGCCTATTATAAGAGACCTTGTGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               653 ACCAGTCTAAACTGAAAGGAGAACTGACCCCCAATCTTCATCCTCCAGAAACCATAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           593 AGGCCCTGAAACCTAGTGTGAAGGTATACGCTGCTGAGCCCTCGAATGCAGATGACTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   773 ATGTCTTCACTGTCACCGAAGATGAAATCAAGTATGCAACCCAGC 817
                                                                                                                                                                                                                                                                                                                       AK026565 4140 bp mRNA linear Homo sapiens cDNA: FLJ22912 fis, clone KAT06132.
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/cell_type="signet-ring cell carcinoma"
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/note="cloning vector pME185FL3"
a 901 c 1050 g 994 t
                                                                                                                                         773 ATGTCTTCACTGTCACCGAAGATGAAATCAAGTATGCAACCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .3e-39;
les 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 181.8;
Pred. No. 5.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:9606"
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AK026565.1 GI:10439447
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88.0%;
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Best Local Similarity 88.0%;
Matches 198; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                                                                                                                       RESULT 15
AK026565/c
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VERSION
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 39 Row: j Column: 10 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 8922495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MAKVADTILFLLDPLEGWDSTGDYCLSCLFAQGLPTYTLAVQGI
SGLPLKKQIDTRKKLSKAVERRFPHDKLLLLDTQQEAGMLLRQLANQKQQHLAFRDRR
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FPLNPRGIRFQKDPDAMEICATDAVDRECLKVLMKADPGRQESLQAEVIPDPMEG
EQTWPTEEELSEAKDFLKEGSKVVKKYPKGTSSYQARAILDGGSQSGGBODEYEYDDM
EHEDFMEEESQDESSEEEEEYETMTIGESVHDDLYDKKVDEEAEAKMLEKYKQERLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact:
    hisc_mgc@nhgri.nih.gov
Shevchenko,X., Werherby,K.D., Becketrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspl,R.,
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McCloskell,J., Pearson,R., Snyder,B., Stantripops,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MFDDEVDTPRDVAARIRFQKYRGLKSFRTSPWDPKENLPQDYARIFQFQNFTNTRKSI
FKEDEEREVEGAEVGWYTLHVSEPVSVVECFRGGTPLLTAFSLLHPBQCMSVLJMVV
RRDFQNTEPVKAKEBLIFHCGFRRFRASPLFSQHTAADKHKLQRFLTADMALYATVYA
PITFPPASVLLFKQKSNGMHSLIATGHLMSVDPDRMVIKRVVLSGHPFKIFTKMAVVR
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VFPKWTYDPYVPEPVPWLKSEISSTVPQGGME"
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          Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                        Direct Submission
Submitted (07-DEC-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                653 ACCAGTCTAAACTGAAAGGAGAACTGACCCCCAATCTTCATCCTCCAGAAACCATAGCAG
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                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site:
http://www.nisc.nih.gov/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="Unknown (protein for MGC:29514)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
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/clone_lib="NIH_MGC_19"
                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 181.8; DB 9;
Pred. No. 5.3e-39;
0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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1. .3807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="DH10B-R"
/note="Vector: pOTB7"
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Compugen Ltd.
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Copyright (c) 1993 - 2003
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                                                AAATCCAGCATTGGCTTGAATACCTGGCCTATTATAAGAGACCTTGTGGATGATGTCTTC
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                        Mothet J,
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(UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
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                       Wolosker
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          The present sequence encodes a mammalian serine racemase, which has a specific activity of at least 0.003 micromole L-serine/mg/hour. The enzyme catalyses the direct racemisation of L-serine to D-serine. D-serine appears to be an endogenous ligand of N-methyl-D-aspartate (NMDA) receptors. The mammalian serine racemases can be used to identify modulators, which can be used in the treatment of acute or chronic neural death or dysfunction mediated by overactivation of N-methyl-D-aspartate (NMDA) receptors. Overactivation of the receptors is associated with Parkinson's disease, Huntington's disease, motor neurone
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                                                                                                                                         Sequence 1672 BP; 491 A; 394 C; 379 G; 408 T; 0 other;
                                                                                                                    disease and Alzheimer's disease.
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CTCATTGAGCCGACTGCTGCGTGCCACTGGCTGCTGTCTCAGCATTTCCAAACA
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                                                                                                                 Serine racemase; N-methyl-D-aspartate receptor; neural death; neural dysfunction; NMDA receptor; Parkinson's disease; Huntington's disease; motor neurone disease; Alzheimer's disease;
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human serine relates to a recombinant polynucleotide encoding a human serine racemase, vectors containing it, host cells expressing the zacemase, methods of identifying inhibitors of serine racemase and a transgenic animal lacking a functional endogenous serine racemase and cracemase, methods of identifying inhibitors of serine racemase and transgenic animal lacking a functional endogenous serine racemase comprising the human serine racemase of the invention. The racemase comprising the human serine racemase of protein, and in structural studies of the protein and sassays to identify compounds that inhibit or stimulate enzyme activity, in the generation of antibodies against the polymentis, and mutant or polymorphic forms of the serine racemase consistents, and mutant or polymorphic forms of the serine racemase (e.g. for neurological diseases such as Parkinson's and Huntingdon's disease, anxiety, glaucoma, stroke, hyperalgesia, pain, spinocerebellar ataxia and sofizophrenia), and would be useful for screening for modulators and/or inhibitors of serine racemase function. The polynucleotides are useful case protein, and as primers for nucleic acid amplification based assays for the detection of polynucleotides encoding cancemase protein. The transgenic animal is useful for the study of the tissue and temporal specific expression or activity of the serine racemase gene in an animal. The gene for human serine racemase is
                                                                                                                                                                                          Human; ss; serine racemase; Parkinson's disease; Huntingdon's disease; anxiety; glaucoma; stroke; hyperalgesia; pain; spinocerebellar ataxia; schizophrenia; transgenic animal; chromosome 17p13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New recombinant serine racemase polypeptide, useful in assays for identifying compounds that alter enzyme activity (e.g. including compounds that inhibit or stimulate enzyme activity) or in generating antibodies against the protein
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Pred. No. 4.1e-247;
0; Mismatches 122; Indels 3;
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                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                      AAS15217 standard; cDNA; 1023
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87.78;
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Best Local Similarity 87.7
Matches 894; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MERI ) MERCK & CO INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Connolly T, Liu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-656991/75
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                                                                        AAS15217;
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RESULT 4
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us-09-889-609b-1.rng

AC AAD14461; XX DT 15-NOV-2001 (first entry) XX DE Human pyridoxal-phosphate dependent enzyme 22406 CDNA.	KW Human; pyridoxal phosphate dependent enzyme; nootropic; neuroprotective; KW anticonvulsant; cerbroprotective; cardiant; vasotropic; gene therapy; KW epilepsy; Alzheimer's disease; chromosome 17; serine racemase; stroke; KW behavioural change; neurodegenerative disorder; schizophrenia; atresia; KW rheumatic heart failure; circulatory disorder; hepatic injury; jaundice;		Key Location/Qualifiers CDS 69.1091 /*tag= a	FT /Product= "Human pyridoxal phosphate dependent enzyme" FT misc_feature 69.1088 FT /*tag= b FT /*tag= b FT /*tag= "This region is specifically claimed as force."	SED 1D NO: 3 WO200160987-A1.	PD 23-AUG-2001. XX XX PF 20-FEB-2001; 2001WO-US05365. XX	PR 17-FEB-2000; 2000US-0183208. XX PA (MILL-) MILLENNIUM PHARM INC. XX	PI Meyers RA, Rudolph-Owen LA: XX XX DR WPI; 2001-529909/58. DR P-PSDB; AAE08342.	XX PT Novel polypeptide of the human pyridoxal phosphate dependent family PT useful in screening and detection assays and for treatment, e.g. of PT epilepsy and Alzheimer's	XX PS Claim 1; Fig 1; 121pp; English. XX CC The present sequence is a CDNA encoding human pyridoxal phosphate		CC Human 22046 and compounds that modulate the expression or activity are CC used to treat or diagnose neurodegenerative disorders including CC Alzheimer's disease, schizophrenia as well as quell anxiety and CC epilepsy and prevent damage from stroke as well as cardiac (heart			Query Match 79.4%; Score 807.8; DB 22; Length 1770; Best Local Similarity 87.7%; Pred. No. 5.5e-247; Matches 894; Conservative 0; Mismatches 122; Indels 3; Gaps 1;
ATGTGTGCTCAGTACTGCATCTCTTGCTGATGTTGAAAAGCTCATATCAACATTCAA 60 	61 GATTCFATCCACCTCACCAGTGCTAACAAGCTCCATTTGAATCAACTAACAGGGGGC 120 121 AATCTTTCTTCAAATGTGAGGCTCTTCCAGAAACTGGGGTCTTTTAAGATTCGAGGTGC 180 121 AATCTTTCTTCAAATGTGAGCTCTTCCAGAAAACTGGGTCTTTTAAGATTCGTGGGTGC 180 121 AATCTTTTCTTCAAATGTGAACTCTTCCAGAAAACAGGATCTTTTAAGATTCGTGGTGCT 180	181 CTTAATGCCATCAGAGGCTTAATTCCTGACACGCCGGAAGAGGAGCCCAAAGCCGTAGTT 240 	241 ACTCACAGCAGGAAACCATGGCCAAGCTCTCACCTATGCTGCTAAACTGGAAGGAA	301 CCTGCTTACATTGTGGTTCCCCAAACAGCTCCCAAGAAGAAGATGGCAATCCAAGCC 360 	361 TATGGAGCATCGATAGTATACTGTGACCCAAGTGACGAGTCCAGAGAAAGGTCACTCAA 420 	421 AGAATTATGCAAGAACAGAAGGCATCTTGGTCCATCCCAACCAGGAGCCTGCAGTGATA 480 	481 GCTGGACAAGGAACATTGCCCTGGAAGTGCTGAACCAGGTTCCCTTGGTAGATGCACTG 540	541 GTGGTACCAGTAGGAGGAGGAATGGTTGCTGGAATAGCCATTACAATTAAGGCCCTG 600 	601 AAACCTAGTGTGAAGGTATACGCTGAGCCCTCGAATGCAGGATGACTGCTACCAGTCT 660 	661 AAACTGAAAGGAGAACTGACCCCCAATCTTCATCCTCCAGAAACCATAGCAGATGGTGTC 720 	721 AAATCCAGCATTGGATTGAATACCTGGCCTATTATAAGAGACCTTGTGGATGATGTCTTC 780 .	781 ACTGTCACCGAAGATGAAATCAAGTATGCAACCCAGCTGGTGTGGGGGAGAATGAAACTG 840 	841 CTCATTGAGCCGACTGCTGGCACTGGCTGCAGTGCTGTCTCAGCATTTCCAAACA 900 	901 GTCTCTCCAGAAGTAAAGAACCTCTGCATTGTACTCAGTGGGGGGAATGTAGACCTAA 958 	959 -CCTCCCTGAACTGGGTGGGGCAGCTGAACGGCCAGCTCCTTACCAGGGGTCTGTTT 1016

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which is a serine racemase. Human 22406 gene is 17 between D17S849 and D17S796. The protein 22406 frine. D serine has been shown to modify sociated with learning, memory and convulsions. dis that modulate the expression or activity are see neurodegenerative disorders including chizophrenia as well as quell anxiety and chizophrenia as well as quell anxiety and triange from stroke as well as cardiac (heart the failure) and circulatory disorders, liver ray, jaundice), lung disorders, prostrate ray, jaundice), lung disorders, prostrate sement, noclular hyperplasia), colon disorders seletal muscle disorders (tumours-rhabdomyosarcoma) disorders. Human 22406 cDNA is also useful in gene
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cDNA encoding human pyridoxal phosphate

    Score 807.8; DB 22; Length 1770;
    Pred. No. 5.5e-247;
    Mismatches 122; Indels 3;

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AAD14461 standard; cDNA; 1770 BP.

RESULT 5
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ID AAD14

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gene therapy;

detection; diagnosis; antisense therapy;

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Yamamoto

Saito K, Otsuki

Nagai K, Hayashi K, A, Nagai K

hikawa T, Wakamatsu Nishikawa

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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
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27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
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             primer;
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                                                                            CCTGCTTACATTGTGGTTCCCCAAACAGCTCCCAACTGCAAGAAACTGGCAATCCAAGCC
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comptrises: (a) an oligo-dT primer and an oligounclectide complementary to the complementary strand of a polynuclectide comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonuclectide comprises at least 15 nucleotides; or (b) a combination of an oligonuclectide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonuclectide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence. Sequence complementary to a journucleotide comprises a 1-end sequence, where the oligonucleotide comprises a 1-end sequence, selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by chefull-length without any specialised methods. AAH133166 to AAH13628 and AAH13633 to AAH13633 to AAH13633 to AAH13633 to AAH13634 to AAH1364 to and a process of the abnormality of the AAH1364 to a particular than a process of the abnormality of the AAH1364 to a particular than a process of the abnormality of the AAH1364 to a particular than a particular than a page and a pa
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87.7%; Pred. No. 6.6e-247;
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                                                                                                              Claim 8; SEQ ID 15148; 2537pp + CD ROM; English
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Matches 894; Conservative
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full-length cDNAs
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Human cDNA sequence SEQ ID NO:15148.

(first entry)

26-JUN-2001

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AAH16282

AAH16282 standard; cDNA; 2477

AAH16282

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Location/Qualifiers 52.1074 /*tag= a

Key

WO200173077-A2

30-MAR-2001;

04 - OCT - 2001

2000US-193748P 2000US-194249P 2001WO-EP03668

03-APR-2000; 31-MAR-2000;

(FARB) BAYER AG

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                             CCTGCTTACATTGTGGTTCCCCAAACAGCTCCCAACTGCAAGAAACTGGCAATCCAAGCC
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Gree AAM50262). The polynucleotide can be used in the production of recombinant serine racemase enzyme, or for the detection of serine racemase enzyme, or for the detection of serine racemase enzyme, or for the detection of serine racemase polynucleotides. Expression vectors and host cells are claimed. Serine racemase arabyses the conversion of L-serine to D-serine. Neuron damage following various nervous system diseases is often caused by activation of gultamate N-methyl-D-aspartate (NMDA) receptors in the brain. This receptor is activated by the binding of D-serine. Regulation of D-serine levels through the regulation of serine racemase may therefore prevent or minimise neuron damage in neurogenic and myopathic disorders, neuron damage in neurogenic and myopathic disorders and Parkinson's disease, and disorders leading to peripheral and enrondegenerative disorders such as Alzheimer's disease and Parkinson's disease, and disorders leading to peripheral and chronic pain. Serine racemase polypeptides and polynucleotides are used in claimed methods of screening for agents that modulate or decrease the activity of serine racemase polynucleotide, or a reagent that modulates serine racemase enzyme activity. This is used to modulate serine racemase enzyme activity. This is used to modulate an enrodegenerative disease caused by the over- or under-activation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polynucleotide encoding serine racemase enzyme and the enzyme useful for screening reagents regulating the activity of the enzyme in a neuron disease caused by over- or under-activation of glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        present sequence is that of cDNA encoding human serine racemase
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Pred. No. 1.5e-246;
0; Mismatches 123; Indels 3;
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Local Similarity 87.6%;
nes 893; Conservative
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                                                                                                                                                                                                                                                                                Score 806.2; DB 22; Length 2674; Pred. No. 2.2e-246; 0; Mismatches 123; Indels 3;
                                                                                                                                                                                                                                                               803 A; 581 C; 563 G; 727 T; 0 other;
                                                                                                                                                                                               (Disclosure); 34pp; Chinese.
                                                                                                                                                               Polypeptide-serine/threonine dehydrase 37 and this polypeptide -
                                                                                                                                                                                                                                                                                  79.28;
87.68;
                                            99CN-0125662
                                                                99CN-0125662
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Best Local Similarity 87.6
Matches 893; Conservative
                                                                                                                                                                                               6; Page 25-26
                                                                                                                               WPI; 2001-530468/59
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          TATGGAGCATCGATAGTATACTGTGACCCAAGTGACGAGTCCAGAGAAAAGGTCACTCAA
                                                                                                                                        AGAATTATGCAAGAAACAGAAGGCATCTTGGTCCATCCCAACCAGGAGCCTGCAGTGATA
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                                                                                                                                                                                                                                                                   full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
              CTCATTGAGCCGACTGCTGGCGTGGCTGCTGCTGTCTCAGCATTTCCAAACA
                                                                                                                                                                                                                                                                                                                       GTCTCTCCAGAAGTAAAGAACGTCTGCATTGTACTCAGTGGGGGGAATGTAGACCTAA--
                                                                                                                                                                                                                                                                                                                                            AAATCCAGCATTGGCTTGAATACCTGGCCTATTATAAGAGACCTTGTGGATGATGTCTTC
                                                                                                                                                                     ACTGTCACCGAAGATGAAATCAAGTATGCAACCCAGCTGGTGTGGGGGAGAATGAAACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                detection; diagnosis; antisense therapy; gene therapy;
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Otsuki 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID 3435; 2537pp + CD ROM; English.
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A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human cDNA clone (5'-primer) SEQ ID NO:3435
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T, Wakamatsu
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99JP-0300253.
2000JP-0118776.
2000JP-0183767.
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, Sugiyama 1
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                sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the comprises a 1'-end sequence, where the complementary is a 1'-end sequence, where the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs casily without any specialised methods. AAH03166 to AAH13628 and AAH13639 to AAH13632 to AAH13632 to AAH13632 to AAH13632 and AAH13633 represent human amino acid sequences; and AAH13632 represent oligonucleotides, all of which are used in the exemplification
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polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 848;
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                                                                                                                                                                                                                                                                                                                                                              Sequence 848 BP; 236 A; 187 C; 214 G; 207 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                        Score 599.6; DB 22;
Pred. No. 1.1e-180;
0; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 58.9%;
Best Local Similarity 87.6%;
Matches 687; Conservative
                                                                                                                                                                                                                                                                                                                     the present invention.
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                                                                                                                                                                                                                                    Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; autidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90044) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the genes are in the nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune discorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (c) cardiovascular disorders such as myocardial ischaemias;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 24; Length 731;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 684; 2081pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 731 BP; 204 A; 158 C; 184 G; 178 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 52.1%; Score 530.4;
Local Similarity 87.7%; Pred. No. 1.3c
Nes 598; Conservative 1; Mismatches
                                                                                                                                                                                                           Human polynucleotide SEQ ID NO 684.
                                                                                                                    BP.
                                                                                                                  ABL90122 standard; cDNA; 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY-2001; 2001WO-US16450.
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                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Birse CE, Rosen CA;
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P-PSDB; ABB89713.
                                      845 ACTG 848
         784
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         ACTG
                                                                                                                                                                             24-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disorders
         781
                                                                                                                                                ABL90122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colitis;
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180
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                                                                                                                                                                                                                                                                                                       480
                                                                                                                                                                                                                                                                                        TATGGAGCATCGATAGTATACTGTGACCCAAGTGACGAGTCCAGAGAAAAGGTCACTCAA 420
                                                                                                                                                                                                                                                                                                                                                             GCTGGACAAGGAACAATTGCCCTGGAAGTGCTGAACCAGGTTCCCTTGGTAGATGCACTG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGGTACCAGTAGGAGGAGGAATGGTTGCTGGAATAGCCATTACAATTAAGGCCCTG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACCTAGTGTGAAGGTATACGCTGCTGAGCCCTCGAATGCAGATGACTGCTACCAGTCT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTCTATCCACCTCACCCCAGTGCTAACAAGCTCCATTTTGAATCAAATAGCAGGGCGC
              AATCTTTTCTTCAAATGTGAGCTCTTCCAGAAAACTGGGTCTTTTAAGATTCGAGGTGCC
                                                                                                               CTTAATGCCATCAGAGGCTTAATTCCTGACACGCCAGAAGAGAAGCCCAAAAGCCGTAGTT
                                                                                                                                                                        CCTGCTTACATTGTGGTTCCCCAAACAGCTCCCAACTGCAAGAAACTGGCAATCCAAGCC
                                                                                                                                                                                                                                                                                                                                               AGAATTATGCAAGAAACAGAAGGCATCTTGGTCCATCCCAACCAGGAGCCTGCAGTGATA
                                                                                                                                                                                                                                                                                                                                                                                                                    Huntington's disease; motor neurone disease; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Serine racemase; N-methyl-D-aspartate receptor; neural death; neural dysfunction; NMDA receptor; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-terminal sequence of human serine racemase DNA.
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99US-0144839.
99US-0145953.
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21-JUL-1999;
28-JUL-1999;
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Best Loca Matches

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5;

Indels

Pred. No. 1.3e-158; 1; Mismatches 81;

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ATGTGTGCTCAGTACTGCATCTCCTTTGCTGATGTTGAAAAAGCTCATATCAACATTCAA

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Ferris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTCTATCCACCTCACCCCAGTGCTAACAAGCTCCATTTTGAATCAAATAGCAGGGGGC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATCTTTTCTTCAAATGTGAGCTCTTCCAGAAAACTGGGTCTTTTAAGATTCGAGGTGCC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAGCTGGACAAGGAACAATTGCCCTGGAAGTGCTGAACCAGGTTCCCTTGGTAGATGCAC 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98
                                                                                           Mammalian serine racemase preparations, used to identify modulators which can be used to treat diseases associated with N-methyl-D-aspartate receptor overactivation, e.g. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGIGICCICAGIACTGCATCICCTITGCTGATGITGAAAAAGCTCATATCAACAITCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              direct racemisation of L.Serine to D.Serine. D.Serine appears to be an endogenous ligand of N-methyl-D-aspartate (NMDA) receptors. The mammalian serine racemases can be used to identify modulators, which can be used in the treatment of acute or chronic neural death or dysfunction mediated by overactivation of N-methyl-D-aspartate (NMDA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 ATGTGCTCAGTATTGCATCTCTTTGCTGAAAAAGCTCATATCAACATTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTCACAGCAGCGGAAACCATGGCCAAGCTCTCACCTATGCTGCTAAACTGGAAGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCTGCTTACATTGTGGTTCCCCAAACAGCTCCCAACTGCAAAACTGGCAATCCAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 TATGGAGCATCGATAGTATACTGTGACCCAAGTGACG-AGTCCAGAGAAAAGGTCACTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA-GAATTATGCAAGAAACAGAAGGCATCTTGGTCCATCCCAACCAGGAGCCTGCAGTGA
                                                                                                                                                                                                                                                                                                      receptors. Overactivation of the receptors is associated with Parkinson's disease, Huntington's disease, motor neurone disease and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                            80;
                                                                                                                                                                                                        racemase gene. The racemase polypeptide has a specific activity o
least 0.003 micromole L-serine/mg/hour. The enzyme catalyses the
                                                                                                                                                                                           The present sequence represents a fragment of a mammalian serine
                            Brady
                                                                                                                                                                                                                                                                                                                                                                                                                    3;
                                                                                                                                                                                                                                                                                                                                                                                         DB 21; Length 608;
                            Mothet J,
                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                             Sequence 608 BP; 174 A; 137 C; 148 G; 148 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGTGGTACCAGTAGGAGG-AGGAGGAATGGTTGCTGGAA 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGTGGNCCCTGTAGGTGGAAGGAGGAATGCTTGCCGGGA
                                                                                                                                                                                                                                                                                                                                                                                      42.7%; Score 434.2; DB 21;
llarity 87.6%; Pred. No. 6.2e-128;
Conservative 0; Mismatches 69;
                           Masaaki T,
JOHNS HOPKINS SCHOOL MEDICINE
                           Sheth K,
                                                                                                                                                                Claim 17; Page 26; 54pp; English.
                           Wolosker H,
                                                                 WPI; 2000-482915/42.
                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 508; Conserv
VINU ( OLYU)
                      SH,
                                         S
                                                                                          Mammalian
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Mammalian serine racemase preparations, used to identify modulators which can be used to treat diseases associated with N-methyl-D-aspartate receptor overactivation, e.g. Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a fragment of a mammalian serine racemase gene. The racemase polypeptide has a specific activity of at direct 0.003 micromole L'serine/mg/hour. The enzyme catalyses the direct racemisation of L-serine to D-serine. D-serine appears to be an endogenous ligand of N-methyl-D-aspartate (NMDA) receptors. The mammalian serine racemases can be used to identify addulators, which can be used in the treatment of acute or chronic neural death or dysfunction mediated by overactivation of N-methyl-D-aspartate (NMDA) receptors. Overactivation of the receptors is associated with Parkinson's disease, Huntington's disease, motor neurone disease and Alzheimer's disease.
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                                                                                                                                                                                                                                          neural dysfunction; NMDA receptor; Parkinson's disease;
Huntington's disease; motor neurone disease; Alzhelmer's disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                              racemase; N-methyl-D-aspartate receptor; neural death;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mothet J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 240.8; DB 21; Length
Pred. No. 3.2e-66;
0; Mismatches 48; Indels
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                                                                                                                                                            C-terminal sequence of human serine racemase DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 18; Page 27; 54pp; English.
  BP.
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99US-0144839.
99US-0145953.
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84.9%;
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                                                                                                       (first entry)
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Best Local Similarity 84.99
Matches 293; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wolosker H,
AAA59296 standard; DNA;
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                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-JAN-2000;
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28-JUL-1999;
                                                                                                       07-NOV-2000
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CD;
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                                                    AAA59296;
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2000US-0241808
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2000US-0242221
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2000US-0240960
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2000US-0246474
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 01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
08-SEP-2000;
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08-NOV-2000;
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                 AAAGAACGTCTGCATTGTACTCAGTGGGGGGAATGTAGACCTAA---CCTCCCTGAACTG 971
                                                                                                                                                                                                                                                                                                                   Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisckling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antiidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
                                                                  GGTGGGGCAGGCTGAACGGCCCAGCTCCTTACCAGACGGTCTGTTT 1016
                                                                                   Human nervous system related polynucleotide SEQ ID NO 8040.
                                                                                                                                                                     ABA15709/c
ID ABA15709 standard; DNA; 20892 BP
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01-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                 Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 GACGAGTCCAGAGAAAGGTCACTCAAAGAATTATGCAAGAAACAGAAGGCATCTTGGTC
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nucleic acid that is a 5' expressed sequence tag (5' EST) for tining cDNAs and genomic DNAs that correspond to 5'ESTs and for mostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                13133 ATATCTTCACTGTCACAGAGGATGAATTAAGGTGAGGCTCCAGC 13089
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                                                                                                                                                                                                                                                                                                                                         Human secreted protein 5' EST, SEQ ID NO: 14944.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity 88.0
Matches 198; Conservative
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are included to maintain the nucleotide numbering
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                                                                                                                                                                                               immunodetection;
                                                                                                                                                                                              Computer readable medium; vaccine; S.aureus infection; immunodetection cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome; toxic shock syndrome; ds.
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are included to maintain the nucleotide numbering
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This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The be used in a vaccine composition against S.aureus infection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelid infections, food poisoning, osteomyelitis, skin and surgical wound infections, scalded skin syndrome, toxic shock syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences C fond their fragments) are useful as primers or probes for isolating commenced to the committee of the S.aureus DNA sequences contained on the Claim 1; Page 452-469; 3271pp; English. computer readable medium. anti-S.aureus vaccines

Sequence 31096 BP; 11857 A; 5243 C; 5477 G; 7488 T; 1031 other;

1321 TGTATTTAAGCCAAAGTATAACTAAAGGGAATGTATTTCTAAAATTAGAAATATGCAAT 1380 1261 TCGAAGAAGCTAAAGCAAGCATTAAACCATTTATTCGTCGAACACCTCTAATTAAATCAA 1320 AGATGAACAAAAAGAAAAAGGCATTATCGCAGCATCTGCTGGGGAACCATGCACAAGGTG 1493 1494 TTGCTTTAACAGCTAAATTATTAGGCATTGATGCAACGATTGTAATGCCTGAAACAGCAC 1553 1674 TTCATCCATATGACGATAAGTTTGTAATGGCAGGCCAAGGAACAATTGGTTTAGAAATTT 1733 1734 TAGATGATATTTGGAATGTGAATACAGTCATCGTACCAGTTGGCGGTGGAGGATTAATTG 1793 CCATTITGAAICAA - - - AIAGCAGGGCGCAAICTITICITCAAAIGTGAGCICITICCAGA 151 152 AAACTGGGTCTTTTAAGATTCGAGGTGCCCTTAATGCCATCAGAGGCTTAATTCCTGACA 211 212 CGCCAGAAGAGGCCCAAAGCCGTAGTTACTCACAGCGGGAAACCATGGCCAAGCTC 271 272 TCACCTATGCTGCTAAACTGGAAGGAATTCCTGCTTACATTGTGGGTTCCCCAAACAGCTC 331 332 CCAACTGCAAGAAACTGGCAATCCAAGCCTATGGAGCATCGATAGTATACTGTGACCCAA 391 392 GTGACGAGTCCAGAGAAAAGGTCACTCAAAGAATTATGCAAGAAACAGAAGGCATCTTGG 451 TCCATCCCÁACCAGGAGCCTGCAGTGATAGCTGGACAAGGAACAATTGCCCTGGAAGTGC 511 TGAACCAGGTTCCCTTGGTAGATGCACTGGTGGTACCAGTAGGAGGAGGAGGAATGGTTG 571 CTGGAATAGCCATTACAATTAAGGCCCTGAAACCTAGTGTGAAGGTATACGCTGCTGAGC 631 CCTCGAATGCAGATGACTGCTACCAGTCTAAACTGAAAGGAGAACTGACCCCCAATCTTC 691 35 TTGAAAAAGCTCATATCAACATTCAAGACTCTATCCACCTCACCCCAGTGCTAACAAGCT Gaps Length 31096; 10; Score 139.8; DB 18; Length Pred. No. 5.4e-33; 0; Mismatches 468; Indels 13.78; Ouery Match Best Local Similarity 48.55 Matches 450; Conservative 1554 1794 95 1434 452 ò a ò op δ op òγ g ò g ŏ g ò QQ οy g δ q Ω q

1854

2094 CTGCAATTTTAAGTGGAAAAATAAACAATAAATGGCTTGAAGATAAAAATGTTGTTGCAT 2153 931 871 692 ATCCTCCAGAAACCATAGCAGATGGTGTCAAATCCAGCATTGGCTTGAATACCTGGCCTA 751 TTATAAGAGACCTTGTGGATGATGTCTTCACTGTCACCGAAGATGAAATCAAGTATGCAA 812 CCCAGCTGGTGTGGGGGAGAATGAAACTGCTCATTGAGCCGACTGCTGGCGTGGCACTGG 2034 TGAAAGATTTAATGCAGCGTGCCAAAATTATTACTGAAGGTGCAGGCGCATTACCAACAG 872 CTGCAGTGCTGTCTCAGCATTTCCAAACAGTCTCTCCAGAAGTAAAGAACGTCTGCATTG 932 TACTCAGTGGGGGGAATGTAGACCTAAC δŻ QQ δλ q Dp δλ Q ò

Search completed: June 24, 2003, 04:26:07 Job time : 291 secs

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Sequence 42, Appl. Sequence 328, Appl Sequence 3283, Appl Sequence 3283, Appl Sequence 6, Appl Sequence 75, Appl Sequence 230, Appl Sequence 261, Appl Sequence 128, Appl Sequence 138, Appl Sequence 14, Appl Sequence 18, Appl Sequence 18, Appl Sequence 28, Appl

US-09-903-180B-6 US-09-903-117A-6 US-09-903-128A-6 US-09-903-322A-6 US-09-903-325A-6 US-09-98-4-761-32574 US-09-98-864-761-32574 US-10-123-155-230

3657 3657 3657 3657 3657

US-09-974-300-2651 US-09-939-980-207 US-09-974-300-1928 US-10-029-217A-6 US-09-759-508B-1 US-10-123-155-196

077 1569 2698 1827 6459 81940 552 569 1956 398

US-09-351-794A-1 US-09-880-107-881 US-10-066-543-522

0 US-09-974-300-271 US-09-918-995-32623 0 US-09-903-187A-6 US-09-903-170C-6

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Sequence 59, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences.
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER REDABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
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REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
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TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 59
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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US-08-781-986A-59
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Sequence 5, Appli
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8031.403 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-804-682-78
US-10-037-270-135
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Maximum Match 100%
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                          64 ATGACAATCGTTCATCCATATGACGATAAGTTTGTAATGGCAGGCCAAGGAACAATTGGT 1723
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                                                                                                                                                                                                                                                1371 AATATGCAATTCACAGGATCTTTTAAATTTAGAGGCGCTAGCAAT-----NAAAATTA 1423
                                                                                                                                          CTAACAAGCTCCATTTTGAATCAA -- - ATAGCAGGGCGCAATCTTTTCTTCAAATGTGAG 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         802 AAGTATGCAACCCAGCTGGTGTGGGGGAGAATGAAACTGCTCATTGAGCCGACTGCTGGC 861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          862 GTGGCACTGGCTGCAGTGCTGTCTCAGCATTTCCAAACAGTCTCTCCAGAAGTAAAGAAC 921
                                                                        84
                                                                     25 TTTGCTGATGTTGAAAAAGCTCATATCAACATTCAAGACTCTATCCACCTCACCCCAGTG
                                                                                                                                                                                                               142 CTCTTCCAGAAAACTGGGTCTTTTAAGATTCGAGGTGCCCTTAATGCCATCAGAGGCTTA
                                                                                                                                                                                                                                                                                  ATTCCTGACACGCCAGAAGAGAAGCCCAAAGCCGTAGTTACTCACAGCAGCGGAAACCAT
                                                                                                                                                                                                                                                                                                                                                      262 GGCCAAGCTCTCACCTATGCTGCTAAACTGGAAGGAATTCCTGCTTACATTGTGGTTCCC
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   Length 31096;
                                      Indels
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14.1%; Score 143.4; DB 7;
48.6%; Pred. No. 1.1e-37;
11ve 0; Mismatches 472;
                                  Conservative
                  Best Local Similarity
Matches 456; Conserv
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TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, TITLE OF INVENTION: Thereof, and Uses Thereof CURRENT APPLICATION NUMBER: US/10/329,960
CURRENT FILING DATE: 2003-01-02
PRIOR APPLICATION NUMBER: US 09/643,990
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: US 08/487,429
PRIOR FILING DATE: 1995-06-07
PRIOR PLICATION NUMBER: US 08/426,787 ပ O U or ororor $^{\rm or}$ or οŗ or $^{\rm or}$ or $^{\rm or}$ or 5 б 5 σ φ б ð b δ ъ 6 Б 5 نہ . نډ نډ ند نہ ORGANISM: Haemophilus influenzae NAME/KEY: misc_feature LOCATION: (45732)..(45732) OTHER INFORMATION: n equals a, a, a, ģ a, ρď NUMBER OF SEQ ID NOS: 1 SOFTWARE: PatentIn version 3.1 NAME/KEY: misc_feature LOCATION: (4747)..(4747) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (9921)..(9921) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (10150)..(10150) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (36543)..(36543) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (36551)..(36551) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (36636)..(36636) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (40808)..(40810) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (44416)..(44416) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (44905)..(44905) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (45593)..(45593) OTHER INFORMATION: n equals APPLICANT: Fleischmann et al NAME/KEY: misc_feature LOCATION: (29298)..(29298) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (44975)..(44975) OTHER INFORMATION: n equals FILE REFERENCE: PB186P1 LENGTH: 1830121 FEATURE:

NAME/KEY: misc_feature

Sequence 1, Application US/10329960 Publication No. US20030099277A1

US-10-329-960-1

RESULT 2

or or or or or or or or or t, g or b ь LOCATION: (47036)..(47036) OTHER INFORMATION: n equals a, t, نہ NAME/KEY: misc_feature LOCATION: (55369)..(55369) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (105121)..(105121) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (117136)..(117136) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (119750)..(119750) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (119924)..(119924) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (120038)..(120038) OTHER INFORMATION: n equals a, a, NAME/KEY: misc_feature LOCATION: (51786)..(51786) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (51805)..(51805) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (65309)..(65309) OTHER INFORMATION: n equals a, LOCATION: (65313)..(65313) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (80024)..(80024) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (100091)..(100091) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (102696)..(102696) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (107248)..(107248) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (121344)..(121344) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (51334)..(51334) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (51602)..(51602) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (122167)..(122167) NAME/KEY: misc_feature FEATURE:

794187 CAGAACAAAAAGCAGCTGGCGTAATAGCAGCCTCTGCGGGTAACCATGCGCAAGGCGTGG 794246 794307 GCATTAAAGTGGATGCAGTGCGTGTTTTGGTGGTGAGGTGTTGTTGCACGGTGCTAATT 794366 215 CAGAAGAGGAAGCCCAAAGCCGTAGTTACTCACAGCAGCGGAAACCATGGCCAAGCTCTCA 274 275 CCTATGCTGCTAAACTGGAAGGAATTCCTGCTTACATTGTGGTTCCCCAAACAGCTCCCCA 334 335 ACTGCAAGAAACTGGCAATCCAAGCCTATGGAGCATCGATAGTATACTGTGACCCAAGTG 394 395 ACGAGTCCAGAGAAAAGGTCACTCAAAGAATTATGCAAGAAACAGAAGGCATCTTGGTCC 454 Gaps Length 1830121; 0 Query Match 8.6%; Score 87.4; DB 9; Length 18 Best Local Similarity 45.7%; Pred. No. 3.9e-17; Matches 304; Conservative 0; Mismatches 361; Indels or or or or or. or g or or or or. t, g or g or ú NAME/KEY: misc_feature LOCATION: (150841)..(150841) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (131340)...(131340) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (131360)..(131360) OTHER INFORMATION: n equals a, FEATURE: NAME/KEY: misc_feature LOCATION: (139910)..(139910) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (142750)..(142750) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (145058)...(145058) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (147197)..(147197) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATTON: (152500). OTHER INFORMATION: n equals a, FEATURE: OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (122336)..(122336) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (145171)..(145171) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (152530)..(152530) NAME/KEY: misc_feature LOCATION: (140398)..(140398) OTHER INFORMATION: n equals FEATURE: NAME/KEY: misc_feature LOCATION: (145942)..(145942) OTHER INFORMATION: n equals FEATURE FEATURE FEATURE FEATURE FEATURE FEATURE FEATURE FEATURE QQ ò ò

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TGCTTACATTGTGGTTCCCCAAACAGCTCCCAACTGCAAGAAACTGGCAATCCAAGCCTA 362
                                                                                                                                                                                                                                                                                                        543 GGTACCAGTAGGAGGAGGAATGGTTGCTGGAATAGCCATTACAATTAAGGCCCTGAA 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: MBARIAM MARIAM MARIAM MAPLICANT: MBARIAM APPLICANT: DeLong, Edward APPLICANT: Beja, Oded APPLICANT: Beja, Oded TITLE OF INVENTION: Light-driven energy generation using proteorhodopsin FILE REFERENCE: MBA-101
CURRENT APPLICATION NUMBER: US/09/847,513A
CURRENT FILING DATE: 2001-05-01
PRIOR PILING DATE: 2000-05-03
                                         284 GGCGACAATTTTTGTATCCGAATCGGTACCGCCTGCCAAACTAGCCGCGCTTCAAGCGAG
                                                                                                                                                                                                                                                      423 AATTATGCAAGAAACAGAAGGCATCTTGGTCCATCCCAACCAGGAGCCTGCAGTGATAGC
                                                                                                                                                                                           CCACTGTCAGCAAACAGGGCAGACGCTCGTCCCACCATTTGACGACGACGACTTATCGC
                                                                                                                                                                                                                                TGGACAAGGAACAATTGCCCTGGAAGTGCTGAACCAGGTTCCCTTGGTAGATGCACTGGT
                                                                              363 TGGAGCATCGATAGTATACTGTGACCCAAGTGACGAGTCCAGAGAAAAGGTCACTCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: gene
LOCATION: (50866)..(51615)
OTHER INFORMATION: Proteorhodopsin gene sequence.
NAME/KEY: misc_feature
LOCATION: (1593)..(3807)
OTHER INFORMATION: Predicted threonine dehydratase.
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Naturally occurring gamma proteobacterium
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Pred. No. 3e-12;
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DATABASE ENTRY DATE: 2000-06-15
RELEVANT RESIDUES: (50866)..(51615)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09847513A; Publication No. US20030104375A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0
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Matches 228; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISSUE: 5486
PAGES: 1902-1906
DATE: 2000-09-15
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VOLUME: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 105184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-847-513A-1
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                         194607 AGGATTCTGCGTGCTTAAAAGGCGCTCTCGATAAAGGCGAACCAACAGATTTAACCCATA 794666
                                                                                                                                                                                                                                                                                                                        GTCAGCAATATCTTCATGATATGGTTGGTCGATAGTGACGAAGTATGCGCAGCAATGA 794786
455 ATCCCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGAACAATTGCCCTGGAAGTGCTGA 514
                                                                                                                                                                                                                          635 CGAATGCAGATGACTGCTACCAGTCTAAACTGAAAGGAGAACTGACCCCCAATCTTCATC 694
                                                                                                                                                                                                                                                                                                    CTCCAGAAACCATAGCAGATGGTGTCAAATCCAGCATTGGCTTGAATACCTGGCCTATTA 754
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                                                                                                                                                    GAATAGCCATTACAATTAAGGCCCTGAAACCTAGTGTGAAGGTATACGCTGCTGAGCCCT
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Fatent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: BERTA, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Expression
FILE REFERENCE: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 8481
SEQ ID NO 4749
LENGTH: 954
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Pred. No. 1.2e-15;
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Best Local Similarity 48.4
Matches 252; Conservative
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; ORGANISM: Bacil
US-09-974-300-4749
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Contains 'n' at position 275
                                                                     AUTHORS: Beja,O., Aravind,L., Koonin,E.V., Suzuki,M.T., Hadd,A.,Nguyen,L.P., AUTHORS: Jovanovich,S.B., Gates,C.M., Feldman,R.A., DeLong,E.F
TITLE: Bacterial rhodopsin: evidence for a new type of phototrophy in the sea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 GGGCGCAATCTTTTCTTCAAATGTGAGCTCTTCCAGAAAACTGGGTCTTTTAAGATTCGA
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167 AGCTCGCAGCTTCGGAAAACGGACTACTCGACCCAACGGTTGGCATCGTCGCGGCATCAG 226
                                        1039544 TCAAAGCAGAGTTCCTCCAAAAGTGCGGCGTGTTCAAAACGCGTGGAGCATTCAACGCC
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Pred. No. 5.2e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAGGAGGAGGAATGGTTGCTGGAATAGC 581
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
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Publication No. US20020197605A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PatentIn ver. 3.0
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HAYASHI, MIKIRO
OCHIAI, KEIKO
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SENOH, AKIHIRO
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                                                          1461 GGAGCGTATAACAAGATTGTAAATTTATCCGATGCC-----GAAAAGAAGAGGGGG 1511
                                                                                                                                            1512 GTTATTGCTGCATCAGCAGAATCATGCTCAAGGGGTAGCCAGTGCATGTAAGAAATTA 1571
                                                                                                                                                                                                                                    1572 AAAATTAATTGCTTGATAGTTATGCCAATAACAACTCCAGAAATAAAAATAAAAGATGTA 1631
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                                                                                                                                                                                                                                                                            355 CAAGCCTATGGAGCATCGATAGTATACTGTGACCCAAGTGACGAGTCCAGAGAAAAGGTC 414
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                  GGTGCCCTTAATGCCATCAGAGGCTTAATTCCTGACACGCCAGAAGAGAAGCCCAAAGCC
                                                                                                   235 GTAGTTACTCACAGCAGCGGAAACCATGGCCAAGCTCTCACCTATGCTGCTAAACTGGAA
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47.2%; Pred. No. 2.7e-13;
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IITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
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Publication No. US20020197605A1
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ANDO, SEIKO
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NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 1091
LENGTH: 930
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OCHIAI, KEIKO
YOKOI, HARUHIKO
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IKEDA, MASATO
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nes 213; Conservative
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US-09-738-626-1091
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	Qy 571 GCTGGAATAGCCATTACAATTAAGGCCCTGAAACCTAGTGTGAAGGTATACGCTGCTGA 629	RESULT 8 US-09-942-891-5 Sequence 5, 7 Sequence 5, 8 Publication P GENERAL INFORMATION APPLICANT: C	; APPLICANT: Kishore, Ganesh Murthy; ; APPLICANT: Slater, Steven Charles ; APPLICANT: Padgette, Stephen Rogers ; APPLICANT: Stark, David Martin ; TITLE OF INVENTION: Methods of Optimizing Substrate Pools and Biosynthesis of ; TITLE OF INVENTION: hydroxybutyrate-co-poly-beta-hydroxyvalerate in Bacteria	EFERENCE: 118 T APPLICATION T FILING DATE APPLICATION N FILING DATE:	POLY-be ; PRIOR and Pla ; PRIOR ; PRIOR ; PRIOR	; PRIOR APPLICATION NUMBER: US 08/614,877 ; PRIOR FILING DATE: 1996-03-13 ; NUMBER OF SEQ ID NOS: 11 ; SOFTWARE: PATEGILIN VERSION 3.1		. ; FEATURE: ; OTHER INFORMATION: Synthetic US-09-942-891-5	Ouery Match 6.0%; Score 60.6; DB 9; Length 1545; Best Local Similarity 46.5%; Pred. No. 7.9e-10; Matches 195; Conservative 0; Mismatches 224; Indels 0; Gaps	Qy 211 ACGCCAGAAGAGCCCAAAGCCGTAGTTACTCACAGCAGGGAAACCATGGCCAAGGT 270	271 CTCACCTATGCTGCTAAACTGGAAGGAATTCCTGCTTACATTGTGGTTCCCCAAACAGCT	Db 280 GTCGCGTTTTCTTCTGCGCGGTTAGGCGTGAAGGCCCTGATCGTTATGCCAACCGCCACC 339 Qy 331 CCCAAGAAACTGCAAGAAATCCAAGCATGGAGCATGGAAGATAGTATTGGAGCATGGATAGAAGTGTGACCCA 390	Db 340 GCCGACATCAAAGTCGACGGCGGCGGCGGGGGGGGGGGG	391 AGTGACGAGTCCAGAGAAAAGGTCACTCAAAGAATTATGCAAGAAAAACAGAAGGCATCTTG	OV 451 GTCCAACCAAGGAGGTGCAGGATGATAGAAAGGAAAAAAATTGCCTGGAAGTGATGATAGTGAAAAATTGCCTGGAAGTG	
	OY 431 AAGAAACAGAAGGCATCTTGGTCCATCCCAACCAGGAGCTGCAGTGATAGCTGGACAAG 490 1039244 CGGAAACTGGTGCTGTTTTGCCACGCCTACGACCAGCCCGACATCGCAGCTGGAGCAG 1039185	Qy 491 GAACAATTGCCCTGGAAGTGCTGAACCAGGTTCCCTTGGTAGATGCACTGGTGGTACCAG 550 Db 1039184 GCGTCATTGGAAAATTGTCGAAGATCTTCCCGACGTTGACACATTGGTG 103912 Qy 551 TAGGAGGAGGAAGAATGTCGTGAATAGC 581 I	Sicon	; APPLICANT: Gruys, Kenneth James ; APPLICANT: Mitsky, Timothy Albert ; APPLICANT: Kishore, Ganesh Murthy ; APPLICANT: Slater, Steven Charles ; APPLICANT: Paddette, Stephen Roqers	APPLICANT: Stark, David Martin TITLE OF INVENTION: Methods of Optimizing Substrate Pools and Biosynthesis of TITLE OF INVENTION: hydroxybutyrate-co-poly-beta-hydroxyvalerate in Bacteria FILE REFERENCE: 11899, 0155, DVUSG		PRIOR APPLICATION PRIOR FILING DATE PRIOR APPLICATION PRIOR FILING DATE	PRIOR APPLICATION NUMBER: US 08/614,877 PRIOR FILING DATE: 1996-03-13 NUMBER OF SEQ ID NOS: 11 SCHEMIANDE, Datonith wording 1	SEQ ID NO 1 LENGTH: 1545 TYPE: DNA	US-09-942-891-1 Query Match 6.0%; Score 60.6; DB 9; Length 1545;	Heer Local Similarity 45.3%; Fred. No. 7.9e-10; Matches 195; Conservative 0; Mismatches 224; Indels 0; Gaps	OY 211 ACCEANAGAGECCEANGCEGITACTTACTCACAGGAGAACATGGCCAAGGT 270 LI	Qy 271 CTCACCTATGCTGCTAAACTGGAAGGAATTCCTGCTTACATTGTGGTTCCCCAAACAGCT 330	280 GTCGCGTTTCTTCTGCGCGGTTAGGCGTGAAGGCCCTGATCGTTATGCCAACCGCCACC	DD 340 GCGGACATCAACGCGGCTGCGCGGCGCGCGAAGTGCTCCAACGCGGCGCGGGGGGAAGTGCTCCACGCGGGGGGGG	

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APPLICANT: Gruys, Kenneth James
APPLICANT: Mitsky, Timothy Albert
APPLICANT: Mitsky, Timothy Albert
APPLICANT: Mitsky, Timothy Albert
APPLICANT: Stater, Ganesh Murthy
APPLICANT: Slater, Steven Charles
APPLICANT: Stark, David Martin
TITLE OF INVENTION: Methods of Optimizing Substrate Pools and Biosynthesis of Poly
TITLE OF INVENTION: Mydroxybutytate-co-poly-beta-hydroxyvalerate in Bacteria and
FILE REFERENCE: 11899, 0155 DVUS02 (MOBT: 155--3)
FILE REFERENCE: 11899, 0155 DVUS02 (MOBT: 155--3)
CURRENT APPLICATION NUMBER: US 09/313,123
PRIOR PELING DATE: 1999-06-17
PRIOR APPLICATION NUMBER: US 08/673,388
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-04-04
PRIOR FILING DATE: 1996-04-04
PRIOR FILING DATE: 1996-03-13
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Pred. No. 7.9e-10;
                                                                                                                                                               Sequence 8, Application US/09942891
Publication No. US20030028917A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Best Local Similarity 46.5
Matches 195; Conservative
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US-09-974-300-264
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APPLICANT: Mitsky, Timothy Albert
APPLICANT: Mitsky, Timothy Albert
APPLICANT: Mitsky, Timothy Albert
APPLICANT: Mitsky, Timothy Albert
APPLICANT: Stark, Ganesh Mutthy
APPLICANT: Stark, David Martin
TILE OF INVENTION: Methods of Optimizing Substrate Pools and Biosynthesis of Poly-be
TITLE OF INVENTION: Methods of Optimizing Substrate Pools and Biosynthesis of Poly-be
TITLE OF INVENTION: Mydroxybutyrate-co-poly-beta-hydroxyvalerate in Bacteria and Pla
TITLE OF INVENTION: Mydroxybutyrate-co-poly-beta-hydroxyvalerate and Pla
TITLE OF INVENTION: Mydroxybutyrate-co-poly-beta-hydroxyvalerate and Pla
TITLE OF INVENTION: Mydroxybutyrate-co-poly-beta-hydroxyvalerate in Bacteria and Pla
TITLE OF INVENTION: Mydroxybutyrate-co-poly-beta-hydroxyvalerate in Bacteria and Pla
TITLE OF INVENTION: Mydroxybutyrate-co-poly-beta-hydroxyvalerate in Bacteria and Pla
PRIOR PLILING DATE: 1996-06-10
PRIOR FILING DATE: 1996-06-28
PRIOR FILING DATE: 1996-04-04
PRIOR FILING DATE: 1996-03-13
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                                                             271 CTCACCTATGCTGCTAAACTGGAAGGAATTCCTGCTTACATTGTGGGTTCCCCAAACAGCT 330
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                          CTGAACCAGGTTCCCTTGGTAGATGCACTGGTGGTACCAGTAGGAGGAGGAGGAATGGTT 570
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                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/09942891 Publication No. US20030028917A1 GENERAL INFORMATION:
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Best Local Similarity 46.5%;
Matches 195; Conservative
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SEQ ID NO 7
LENGTH: 1545
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                                            726 CAGCATTGGCTTGAATACCTGGCCTATTATAAAGAGACCTTGTGGGATGATGTCTTCACTGT
                                                                                                                                                                                                                                                                                                              APPLICANT: Perret, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
TITLE OF INVENTION: Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 CCATTTTGAATCAAATAGCAGGGGGCGCAATCTTTTCTTCAAATGTGAGGCTCTTCCAGAAA
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                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: CARPOOG8
CURRENT APPLICATION NUMBER: US/09/939,964
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 09/214,808
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                           Sequence 1, Application US/09939964 Publication No. US20030054522A1 GENERAL INFORMATION: APPLICANT: Rosenthal, Andre
                                                                                                                                                                                                                                                                                                     Christoph
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Best Local Similarity 44.5%;
Matches 263; Conservative
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US-09-939-964-1
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 CATCTCCTTTGCTGATGTTGAAAAGCTCATATCAACATTCAAGACTCTATCCACCTCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1251;
                                                                                      TITLE OF INVENTION: Methods For Monitoring Multiple Gene TITLE OF INVENTION: Expression FILE REFERENCE: 10085.500-09: CURRENT APPLICATION NUMBER: US/09/974,300 CURRENT FILING DATE: 2001-10-05 PRIOR PRILCATION NUMBER: 09/680,598 PRIOR FILING DATE: 2000-10-06 PRIOR FILING DATE: 2000-10-06 PRIOR FILING DATE: 2001-03-27 NUMBER OF SEQ ID NOS: 8481 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches 413;
                                                                                                                                                                                                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                             Score 55.2; DB 1(
Pred. No. 5.2e-08;
Sequence 264, Application US/09974300
Patent No. US20020146721A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Bacillus licheniformis
US-09-974-300-264
                                                                                                                                                                                                                                                                                                                                                                                                               5.4%;
                                                       APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
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Best Local Similarity 44.99
Matches 354; Conservative
                                                                                                                                                                                                                                                                                                                      LENGTH: 1251
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                                                                                                                                                                                                                                                                657 GTTGAGTTAGACGAAAATCGACAAATTTGTCGATGGAGGGGCTGTGAAAAAAGTCGGCGAC 716
                                                                                                                                                                                                                                                                                                                  AATACCTGGCCTATTATAAGAGACCTTGTGGATGATGTCTTCACTGTCACCGAAGATGAA 798
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                                                          537 GGTGGGCTTATTAGTGGGATGGCCACGTATAAAAAAGCGTTAGCCCAACTACGAAAATG
          GGAGGAATGGTTGCTGGAATAGCCCATTACAATTAAGGCCCTGAAACCTAGTGTGAAGGTA
                                                                                                         619 TACGCTGCTGAGCCCTCGAATGCAGATGACTGCTACCAGTCTAAACTGAAAGGAGAACTG
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TITLE OF INVENTION: No. US20020197679Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 38.8; DB 9; Length 1
Pred. No. 0.027;
0; Mismatches 137; Indels
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CURRENT APPLICATION NUMBER: US/10/098,841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2002-03-13
PRIOR APPLICATION NUMBER: 09/598,042
PRIOR FILING DATE: 2000-06-20
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PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 331
SOFTWARE: PL_FLGENES VERSION 1.0
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o. US20020197679A1
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Best Local Similarity 49.0%;
Matches 143; Conservative (
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Qian, Xiaohong B.
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Chen, Rui-hong
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Xu, Chongjun
Zhou, Ping
Ma, Yunqing
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Zhao, Qing A.
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APPLICANT: Liu, Chenghua
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; LOCATION: (182)..(1171)
US-10-098-841-197
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| AT 778
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Length 926;
                                                                                                                                                                      Sequence 4809, Application US/09974300
Fatent No. US20020146721A1
GENERAL INFORMATION:
APPLICANT: Berka. Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: WHERE: US/09/974,300
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT APPLICATION NUMBER: 09/680,598
PRIOR APPLICATION NUMBER: 60/279,526
PRIOR FILING DATE: 2000-10-06
PRIOR FILING DATE: 2000-10-37
NUMBER OF SEQ ID NOS: 8481
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44.2%; Pred. No. 6.6e-05;
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LOCATION: (1)...(926)
OTHER INFORMATION: n = A,T,C or G
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Matches 346; Conservative
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LENGTH: 926
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13652 AAAGAAATGCTAGAACAAGCAAAGTCTGACAATGTTAACTTTGATTATCTATTTGCCGCA 13711
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                                                                                                                                                                            13532 ACTGGTGATACATTTGATCACTGTTTAGCTGAAGCTTTAACTTATACAAGTGAACATCAA 13591
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                                                                                                                                                                                                                                           CCCAACTGCAAGAAACTGGCAATCCAAGCCTATGGAGCATCGATAGTATACTGTGACCCA
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                                                                                               TCAGATGAAGCTAAAAGTAAAGGTATTACATGTGCAAGTGCAGGTAATCATGCTCAAGGT
                                                                                                                                              271 CTCACCTATGCTGCTAAACTGGAAGGAATTCCTGCTTACATTGTGGTTCCCCAAACAGCT
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Job time : 211 secs
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GAATCAAATAGCAGGGGGCAATCTTTTTTTCTTCAAATGTGAGCTCTTCCAGAAAACTGGGTC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 102, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5.555
CORRESPONDENCE ADDRESS:
                                                                                             162 TTTTAAGATTCGAGGTGCCCTTAATGCCATCAGAGGCTTAATTCCTGACACGCCAGAAGA
                                                                                                                                                                                        222 GAAGCCCAAAGCCGTAGTTACTCACAGCGGAAACCATGGCCAAGCTCTCACCTATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31 GATGTTGAAAAAGCTCATATCAACATTCAAGACTCTATCCACCCTCACCCCAGTGCTAACA
                                                                                                                                                                                                                                                                                   282 TGCTAAACTGGAAGGAATTCCTGCTTACATTGTGGTTCCCCAAACAGCTCCC 333
                                                                                                                                                                                                                                                                                                                Length 15249;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette: 3.50 inch, 1.4mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS VERSION 6.2 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 38.4; DB 7;
Pred. No. 0.17;
0; Mismatches 406;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEPAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 15249 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 44.7'
Matches 355; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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US-08-781-986A-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-08-781-986A-102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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June 24, 2003, 05:11:01; Search time 276.093 Seconds (without alignments) 132.862 Million cell updates/sec
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/ cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*

/ cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

/ cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

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/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417779 segs, 108206813 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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Maximum DB :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Description	Sequence 4591, Ap	Sequence 5828, Ap	Sequence 13657, A	Sequence 6317, Ap	Sequence 32, Appl	Sequence 10707, A	Sequence 10239, A	Sequence 65, Appl	Sequence 13862, A	Sequence 31, Appl	Sequence 66, Appl	Sequence 62, Appl	Sequence 12146, A	Sequence 12800, A	Sequence 5437, Ap	Sequence 64, Appl	Sequence 4, Appli	Sequence 11879, A	Sequence 11179, A
QI	US-09-738-626-4591	US-09-738-626-5828	US-09-815-242-13657	US-09-738-626-6317	US-09-931-457A-32	US-09-815-242-10707	US-09-815-242-10239	US-09-931-457A-65	US-09-815-242-13862	US-09-931-457A-31	US-09-931-457A-66	US-09-931-457A-62	US-09-815-242-12146	US-09-815-242-12800	US-09-815-242-5437	US-09-931-457A-64	US-09-905-290A-4	US-09-815-242-11879	US-09-815-242-11179
DB	6	σ	10	6	0	10	10	σ	10	6	6	0	10	10	10	δ	6	10	10
% Query Match Length DB	310	436	306	308	325	310	323	383	323	325	386	398	313	313	303	415	324	324	316
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Score	357.5	307	201.5	196	177	175.5	168	167	161	160.5	160.5	160	159.5	159.5	157.5	157	156.5	154.5	143.5
Result No.	П	7	٣	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19

6

41;

DB 9; Length 310; Indels

20.5%; Score 357.5; DB 9; 30.3%; Pred. No. 2.5e-25; iive 52; Mismatches 139;

Query Match
Best Local Similarity 30.39
Matches 101; Conservative

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28

63 -AIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAY 121

7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALN----

Sequence 5737, Ap Sequence 5135, A Sequence 11535, A Sequence 11535, A Sequence 11535, A Sequence 21, Appli Sequence 22, Appli Sequence 22, Appli Sequence 24, Appli Sequence 24, Appli Sequence 25, Appli Sequence 6, Appli Sequence 6, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 13, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli	
10 US-09-815-242-5737 10 US-09-815-242-11292 10 US-09-738-626-5818 10 US-09-738-626-5818 10 US-09-759-5081-2 10 US-09-759-5081-2 10 US-09-759-5081-2 10 US-09-734-017A-28 9 US-09-734-017A-28 9 US-09-734-017A-24 10 US-09-734-017A-24 9 US-09-734-017A-24 10 US-09-734-017-6 9 US-09-734-017-6 9 US-09-742-096-5 9 US-09-117-417-6 9 US-09-914-947A-20 10 US-09-914-947A-20 10 US-09-914-947A-20 10 US-09-914-9133 9 US-09-997-181-133 9 US-09-997-181-133 9 US-09-997-182-133 10 US-09-997-182-133 10 US-09-997-182-133	ALIGNMENTS 1-626-4591 Ee 4591, Application US/09738626 tion No. US20020197605A1 ANT: NAKAGAWA, SATOSHI ANT: NAKAGAWA, SATOSHI ANT: NAKAGAWA, SATOSHI ANT: HAYASHI, HIROSHI ANT: ANDO. SEIRO ANT: OCHIAL, MKIRO ANT: OCHIAL, KEIKO ANT: TATELSHI, NAOKO ANT: OCHIAL ANDELCATION NUMBER: US/09/138,626 TELING DATE: 2000-12-16 APPLICATION NUMBER: US 00/159162 FILING DATE: 2000-04-07 FILING DATE: 2000-04-07 FILING DATE: 2000-04-07 FILING DATE: 2000-08-03 RE: PATENTIN VER: 3.0 NO 4591 H: RT ISM: COLYNOBACLETIUM Glutamicum
314 10 316 10 316 10 2550 10 26853 10 1682 10 1682 10 2284 9 202 10 202 10 203 9 204 9 204 9 204 10 205 9 207 10 209 10 2	Dlication US/05 220020197605A1 NA, SATOSHI UCHI, HIROSHI SEIKO II, KEIKO II, KEIKO II, KEIKO II, KEIKO II, MASATO II, MASATO II, AKIO NN: NOVEL POLYN AS 1200-12-16 A NUMBER: JP 99 3: 2000-04-17-16 A NUMBER: JP 90 3: 2000-04-17-16 III NUMBER: JP 90 3: 2000-04-17-16 III VORS: 7059 IN VORS: 7059 IN VORS: 7059
	ALIG ULT 1 Gquence 4591, Application US/09738626 ublication No. US20020197605A1 ENERAL INFORMATION: APPLICANT: NARAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSHI APPLICANT: ANDO, SEIKO APPLICANT: ANDO, SEIKO APPLICANT: ANDO, SEIKO APPLICANT: TYEISHI, MIRRO APPLICANT: TYEISHI, MIRRO APPLICANT: TYEISHI, MACKO APPLICANT: TYEISHI, NACKO APPLICANT: TYEISHI, NACKO APPLICANT: TYEISHI, NACKO APPLICANT: TYEISHI, NACKO APPLICANT: GANDI, AKIHRO APPLICANT: LANDO TITLE OF INVERTION: NOVEL POLYNUCLEOT FILE REFERENCE: 249-12-18 PRIOR APPLICATION NUMBER: JP 99/37748 PRIOR FILING DATE: 1999-12-16 PRIOR APPLICATION NUMBER: JP 00/15916 PRIOR FILING DATE: 2000-04-07 PRIOR APPLICATION NUMBER: JP 00/28098 PRIOR FILING DATE: 2000-04-07 PRIOR APPLICATION NUMBER: JP 00/28098 PRIOR FILING DATE: 2000-04-07 PRIOR APPLICATION NUMBER: JP 00/28098 PRIOR FILING DATE: 2000-08-03 NUMBER OF SEO ID NOS: 7059 SOFTWARE: PREGETTIN VET: 3.0 LENGTH: 310 TYPE: PRE
141.5 11129 1111.5 1111.5 1111.5 1110.5 1100.5 1	SULT 1 Sequence 4591, Appl. Sequence 4591, Appl. GENERAL INFORMATION APPLICANT: NAZAGAW: APPLICANT: MIZOGU APPLICANT: MIZOGU APPLICANT: TATEGU APPLICANT: CCHAI APPLICANT: CCHAI APPLICANT: COURLAI APPLICANT: COURLAI APPLICANT: CORNEY APPLICANT: TATEGO APPLICANT: TREDA, APPLICANT: CORNEY APPLICANT: CORNEY APPLICANT: DAY PRIOR PETLING DATE: PRIOR FILING DATE: PRIOR FILING DATE: PRIOR APPLICATION PRIOR APPLICATION PRIOR FILING DATE: PRIOR APPLICATION OF SEQ ID NG SEG ID
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240 VK-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQL--VWGRMKLLIEPTAGVALAAVLSQ 296
                                                                             257 AAVKRVGDLNYTIVEKNQGRVHMMSATEGAVCTEMLDLYQNEGIIAEPAGALSIAGLKEM 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 AVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPSDESREK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 V - TQRIMQETEGILVHPNQEPA - - - - - - - VIAGQGTIALEVLNQVPLVDALVVP 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELTRA.OILA
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT APPLICATION NUMBER: 00.01.018
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,348
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PRILOR TOWNER: 60/257,931
PRIOR PRILOR DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                               297 HFQTVSPEVKNVCIVLSGGNVDLTSLNWVGQAER 330
                                                                                                                                                                                                          Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13657
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ohlsen, Kari L.
Zyskind, Judith W.
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28.1%; Pred. No. 2.2e-20;
Live 58; Mismatches 162;
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CURRENT FILING DATE: 2000-12-18
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PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
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Publication No. US20020197605A1
GENERAL INFORMATION:
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ANDO, SETKO
HAYASHI, MKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TAMEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
OZAKI, AKIO
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Best Local Similarity 28.1%
Matches 94; Conservative
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                                                                                                                                                                                                                                                                                                                 70;
                                                                                                                                                                                                                                                                      Length 325;
                                                                                                                                                                                                                                                                                                                 Indels
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                 Query Match 10.2%; Score 177; DB 9; L
Best Local Similarity 23.9%; Pred. No. 2.2e-08;
Matches 74; Conservative 53; Mismatches 112;
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10707, Application US/09815242 Patent No. US20020061569A1
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APPLICATION WUMBER: 60/207,727
APPLICATION NUMBER: 60/207,727
APPLICATION NUMBER: 60/242,578
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APPLICATION NUMBER: 60/269,308
FILING DATE: 2001-02-16
                             60/049,406
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APPLICATION NUMBER: 60/253,625
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APPLICATION NUMBER: 60/257,931
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Trawick, John D. Carr, Grant J. Yamamoto, Robert T.
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/C
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 72
SOFTWARE: MICROSOFT OFFICE 97
                                                                                                                                                                                            ; ORGANISM: Citrullus lanatus
US-09-931-457A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
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273 SGAAAAAI 281
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LENGTH: 325
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                                                                                                                                                                      TYPE: PRT
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APPLICANT: Falco, S. Carl
APPLICANT: Allen, Stephen M.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
CURRENT APPLICATION NUMBER: US/09/931,457A
PRIOR APPLICATION NUMBER: 09/424,976
PRIOR FILING DATE: 1999-112-02
PRIOR APPLICATION NUMBER: 60/065,385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35; Mismatches 109;
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR PELICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PALENTIN VET: 3.0
                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                  Sequence 6317, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
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US-09-738-626-6317
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                                                                                                                                                                 MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                          YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIKO
IKEDA, MASATO
OZAKI, AKIO
                                                                                                                                          APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                       ANDO, SEIKO
HAYASHI, MIKIRO
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Best Local Similarity 28.49
Matches 80; Conservative
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APPLICANT:
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66 VEPTSGNTGIALAYVAAARGYKLTLTMPETMSIERRKLLKALGANLVLTEGA-----KGM 120
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                                                                                                                                                                                                                                                                                                                                                                                                               140 QRIMQETEGILVHPNQEPAVIAGQ------GTIALEVLNQVP-LVDALVVPVGG 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 KLESMEPCCSVKDRIGYSMI-----DDAEQKGVITPGKTTLVEPTSGNTGLGLAFIAAAR 151
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                                                                                                                  26 TPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAI-----RGLIPDTPEEKPKA-V 79
                                                                                                                                                                                          15 TPLVR---LNRIGNGRILAKVESRNPSFSVKCRIGANMIWDAEKRGVL-----KPGVEL 65
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                                             Indels
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TITLE OF INVENTION Plant Amino Acid Biosynthetic Enzymes FILLE REFERENCE: BB116 US CIP CURRENT APPLICATION NUMBER: US/09/931,457A CURRENT FILLING DATE: 2002-02-22 PRIOR APPLICATION NUMBER: 09/424,976 PRIOR FILING DATE: 1999-12-02
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Best Local Similarity 25.3%; Pred. No. 1.5e-07;
Matches 78; Conservative 53; Mismatches 133;
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SOFTWARE: Microsoft Office 97
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292 NKNIVVIL 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |: :| : | :: | ||: : | ||: | ||: | ||: | ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68 TIIEPTSGNTGIGLAMVGAALGYPVKIVMPDIMSIERRKLMQAYGADLLLIFPGAEGMKGA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 VTQ-RIMQETEGI---LVHPNQEPAVIAGQ--GTIALEVLNQVPLVDALVVPVGGGGMVA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSSIGLNTWPI 251
                                                                                                                                                                                                                                                                                                                                                                                                        18 NIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYTELIGOSPVVKLKRMVPEGAADVFVKLEFFNPGGSVKDRIALSMIQQAEADGRLKPGQ 67
                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                               DB 10; Length 310;
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                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --TVYQKVAAVSSEDALETARLMGPKEGILVGISAGAAIKAAI 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 IRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVL 294
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                       10.1%; Score 175.5; DB 10; 24.7%; Pred. No. 2.9e-08; tive 55; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 168;
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 10707
LENGTH: 310
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10239
LENGTH: 323
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PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR FILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-110-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
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Patent No. US20020061569A1
                                                                                                                                            ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
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Carr, Grant J.
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Matches 70; Conservative
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US-09-815-242-10239
                                                                                                                                                                               US-09-815-242-10707
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241 LK-----LIDKVVGITNEEAISTARRLMEEGGILAGISSGAAVAAALKLQ-EDESFTN 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 GASIVYCDPSDESREKVTQRIMQETEGILVH-PNQEPAVIAGQ-------GTIALE 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 V-LNQVPLVDALVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222 GPHKIQGIGAĞFIPGVLEVN-----LLDEVVQISSDBAIETAKLLALKEGLFVGISSG 274
246 LNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 NLHPPETIADG-VKSSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VERSGIAKDVTELIGKTPLV---YLNKLADGCVARVAAKLELMEPCSSVKDRIGYSMIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12 VEKAHI--NIQDSIHLTPVLTSSILNQIAG---RNLFFKCELFQKTGSFKIRGALNAI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 325;
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Falco, S. Carl.
APPLICANT: Falco, S. Carl.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
TITLE OF INVENTION BELLIG CIP
CURRENT APPLICATION NUMBER: US/09/931,457A
CURRENT FILING DATE: 2002-02-22
PRIOR PPLICATION NUMBER: 09/424,976
PRIOR APPLICATION NUMBER: 60/065,385
PRIOR APPLICATION NUMBER: 60/065,385
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
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APPLICANT: Allen, Stephen M.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
FILE REFERENCE: BB1116 US CIP
CURRENT APPLICATION NUMBER: US/09/931,457A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54; Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .8e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.2%; Score 160.5; 25.5%; Pred. No. 7.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 VALAAVLSQHFQTVS-PEVKNVCIV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 AAAAAA - - - FOIAKRPENAGKLIV 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 66, Application US/09931457A Patent No. US20020157132A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                   ; Sequence 31, Application US/09931457A
; Patent No. US20020157132A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 72
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Glycine max
                                                                                               306 KNVCIVL 312
                                                                                                                                          293 KNIVVIL 299
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Best Local Similarity
Matches 83; Conserv
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                                                                                                                                                                                                                     RESULT 10
US-09-931-457A-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRIMQETEGILVHPNQEPAVI-----AGQGTIALEVLNQVP-LVDALVVPVGGGG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 KGAIQKAEEIVASDPOKYLLLOQFSXPANPEIHEKTTGPEIWEDTDGQVDVFISGVGTGG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MVAGIAITIKALKPSVKV--YAAEPSNADDCYQSKLKGELTPNLHPPETIADG-VKSSIG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 ADDCYQSKLKGELTPNLHPPETIADG-VKSSIGLNTWPIIRDLVDDVFTVTEDE-IKYAT 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 TPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAI-----RGLIPDTPEEKPKA-V 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 TPLVR----LNRIGNGRILAKVESRNPSFSVKCRIGANMIWDAEKRGVL-----KPGVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.OILA
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT PAPLICATION NUMBER: 00/19,078
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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9.3%; Score 161; DB 10;
Best Local Similarity 24.1%; Pred. No. 6.9e-07;
Matches 74; Conservative 55; Mismatches 136;
                                                ----ESNILSGGKPGPHKIQGLGAGFVPSNLDLG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OS SEQ ID NOS: 14110
SOFFWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (1)...(323)
OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                           272 QLVWGRMK - - LLIEPTAGVALAAVL 294
                                                                                                                                                                                                                                                                   Sequence 13862, Application US/09815242 Patent No. US20020061569A1
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                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari E.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                   : Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT
                                                                                                                                                                                                                                            09-815-242-13862
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APPLICANT: Haselbeck, Robert
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Trawick, John D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 SSTEIEGLNIAEDVTQLIGNTPMV---YLNTIAKGCVANIAAKLEIMEPCCSVKDRIGFS 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 AI-----RGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 IQAYGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVP-- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LVDALVVPVGGGGMVAGIAITIKALKPSVKV 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 IGVEPTESNVLSGGK------PGPHKIQGIGAGFIPGNLD------QDVMDEVIEISSD 313
                                                                                                                                                                                                                                                                                                                                                                                                                                           8 SFADVEKAHI---NIQDSIHLTPVLTSSILNQIAG---RNLFFKCELFQKTGSFKIRGALN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 YAAEPSNADDCYQSKLKGELTPNLHPPETIADG-VKSSIGLNTWPIIRDLVDDVFTVTED
                                                                                                                                                                                                                                                                                                                                                 Length 386;
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Best Local Similarity 24.4%; Pred. No. 1.2e-06;
Matches 69; Conservative 56; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Allen, Stephen M.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
FILE REFERENCE: BB1116 US CIP
CURRENT APPLICATION NUMBER: US/09/931,457A
CURRENT FILING DATE: 2002-02-22
                                                                                                                                                                                                                                                                                                                                                 Score 160.5; DB 9;
Pred. No. 1e-06;
                                                                                                                                                                                                                                                                                                                                                                                              59; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                266 EIKYATQLVWGRMKLLIEPTAG-VALAAV 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   314 EAVETARTLALQEGLLVGISSGAAALAAI 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/424,976
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/065,385
PRIOR PLILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/049,406
PRIOR PLILING DATE: 1997-06-12
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/424,976
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/065,385
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/049,406
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 72
SOFTWARR: MICROSOÍT OÍTICE 97
SEQ ID NO 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
US-09-931-457A-62
Gequence 62, Application US/09931457A
Facent No. US20020157132A1
                                                                                                                                                                                                                                                                                                                                               Query Match 9.2%;
Best Local Similarity 21.6%;
Matches 71; Conservative 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 72
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                               ORGANISM: Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CORGANISM: Zea mays
US-09-931-457A-62
                                                                                                                                                                                                                                                                                                    US-09-931-457A-66
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12;

Gaps

34;

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136 - EKVTQRIMQETEGILVHPNQEPA-VIAGQGTIALEVL-NQVPLVDALVVPVGGGGWVAG 192
                                                                                                                                                                                                                                                                 205 LDKATEILNKTPNSYMLQQFDNPANPQVHYETTGPEIWEDSKGKVDIFIGGIGTGGTISG 264
                                                                                                                                                                                                                                                                                                                            193 IAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSSIGLNTWPII 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 FLMAQKPVDNITQIIGGTPVVKLRNVVDDNAADVYVKLEYQNPGGSVKDRIALAMIEKAE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9 FADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFOKTGSFKIRGALNAIRGLI 68
23 IHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAI-----RGLIPDTPEEKPK 77
                                                                                                          78 AVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPSDESR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      253 RDLVDDVFTVTEDE-IKYATQLVWGRMKLLIEPTAGVALAAVL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes in TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10;
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9.2%; Score 159.5; DB
Best Local Similarity 23.6%; Pred. No. 9.1e-07
Matches 70; Conservative 52; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organisms 12.44. Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFLIGHT DATE: 2000-05-26

REPLING DATE: 2000-05-26

REFLING DATE: 2000-10-23

REPLING DATE: 2000-110-27

REPLING DATE: 2000-111-27

REPLING DATE: 2000-111-27

REPLING DATE: 2000-111-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-12-22
APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Staphylococcus aureus
US-09-815-242-12146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Carr, Grant J.
Yamamoto, Robert T.
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138 VTQ-RIMQETEGILVHPNQ-----EPAVIAGQGTIALEVLNQV--PLVDALVVPVGGGGM 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            190 VAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSSIGLNTW 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78 AVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPSDESREK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 NIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 NITQIIGGTPVVKLRNVVDDNAADVYVKLEYQNPGGSVKDRIALAMIEKAEREGKIKPGD 61
23;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                              OM protein - protein search, using sw model
                                                                                                                                          Run on:
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June 24, 2003, 06:07:29; Search time 26.9602 Seconds (without alignments) 1208.801 Million cell updates/sec US-09-889-609B-8 1740 1 MCAQYCISFADVEKAHINIQ.....TSLNWVGQAERPAPYQTVSV 339

Title: Perfect score: Sequence: Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

SUMMARIES

	Description	probable threonine	threonine ammonia-	threonine ammonia-	L-serine ammonia-1	threonine ammonia-	threonine ammonia-	threonine ammonia-	probable serine/th	threonine dehydrat	probable threonine	threonine ammonia-	hypothetical prote	threonine dehydrat		threonine ammonia-	threonine dehydrat	threonine ammonia-	probable threonine	threonine ammonia-	threonine dehydrat	threonine dehydrat	hypothetical prote	probable threonine	threonine ammonia-					
	ID	T04211	S38061	T41297	E83310	F89921	T36434	D72386	A97687	AF2912	F95390	T24337	D90166	G87633	H84359	AB0897	DWECTD	D85973	E91128	AG0496	D97778	F83603	D81355	H71703	E75502	A87700	AC3142	T23166	B95894	T39516
	DB	7	7	~	7	7	7	7	7	7	7	7	7	7	7	7	٦	7	7	7	7	7	7	7	7	7	7	7	7	7
	Length	,				346											329							333			33	512	334	009
æ	Match	45.5	33.7	32.2	31.3	30.7	30.5	30.0	29.9	29.9	29.7	29.5	28.7	28.6	28.3	28.2	27.4	27.4	27.4	26.8	26.8	26.6	25.7	. 25.5	25.4	25.2	24.5	24.3	23.8	23.7
	Score	791				535	_			'n	517.5	'n.	66	S.			476		9/		66.5	s.	s.	44.5	0	33	'n	423	414	413
4	NO.	7	7	m	4	S	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	. 23	24	25	56	27	28	29

RESULT 2 S38061

threonine ammonia-	threonine dehydrat	probable threonin	probable threonine	threonine ammonia-	threonine dehydrat										
877559	B83479	A98146	C72630	AG0474	DWBYT	E82374	AB0924	B91217	DWEBTT	C86063	DWECTS	A69644	A38628	T51712	AF1839
7	7	7	7	~	-	7	7	7	-	7		7	7	7	7
508	515	304	349	514	576	510	514	514	514	515	514	422	595	592	257
5.	23.4	23.2	22.9	22.9	22.7	22.5	22.1	22.0	21.8	21.8	21.7	21.5	21.4	21.3	21.1
. 23		s.	661	398	5.5	391	384	382	380	78.5	378	374	71.5	371	368
	406.5	403	(*)	• •	39					'n			'n		

ALIGNMENTS

RESULT 1 T04211 probable threonine ammonia-lyase (EC 4.3.1.19) T5C23.70 [similarity] - Arabidopsis th	Species: Arabidopsis thaliana (mouse-ear cress) ande: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jun-2002 Accession: T04211	Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancrc Idmitted to the Protein Sequence Database, March 1999 Reference number: 215561	Accession: T04211 Molecule type: DNA	:Residues: 1-346 <bev> :Cross-references: EMBL:AL049500</bev>	Experimental source: cultivar Columbia; BAC clone T5C23	; Map position: 4	.introns: 55/2; 99/2; 176/2; 263/2 .Note: T5C23.70	;Superfamily: threonine dehydratase ;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase	Query Match 45.5%; Score 791; DB 2; Length 346;	Matches 159; Conservative 68; Mismatches 88; Indels 24; Gaps 6;							169	184						RESULT TO A 211 TO A	1 threonine ammonia-lyase (EC 4.3.1.19) T5C23.70 [similarity] - Arabidopsis less arabidopsis thaliana (mouse-ear cress) 1.30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jun-2002 1.30-Apr-1999 #sequence_revision 30-Apr-1999 1.30-Apr-1999 1.30-Apr-1999 #sequence_revision 30-Apr-1999 1.30-Apr-1999 1.
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Gaps

14;

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A;Residues: 1320 <GTO>
A;Cross-references: GB:AE004696; GB:AE004091; NID:g9948750; PIDN:AAG06071.1; GSPDB:GN
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                              A;Cross-references: EMBL:AL031603; PIDN:CAA20920.1; GSPDB:GN00068: SPDB:SPCC330.15c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L'serine ammonia-lyase (EC 4.3.1.17) [similarity] - Pseudomonas aeruginosa (strain C; Species: Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa C; Species: D-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 21-Jun-2002 C; Accession: E83310 R: Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                           C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 IPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDPSDESREKVTQRIMQETEGI-LVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 YDRYKDDREKMAKEI-SEREGLTIIPPYDHPHVLAGQGTAAKELFEEVGPLDALFVCLGG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSS-IG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ||:::||:::||:::|
185 GGLLSGSALAARHFAPNCEVYGVEPPEAGNDGQQSFRKGSIV-HIDTPKTIADGAQTQHLG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8 SFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGL
                 Wambutt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 323;
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           R;Gwilliam, R.; Barrell, B.G.; Rajandream, M.A.; Wedler, H.;
submitted to the EMBL Data Library, September 1998
A;Reference number: 221987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 32.2%; Score 560; DB 2; Best Local Similarity 39.6%; Pred. No. 2.6e-36; Matches 125; Conservative 68; Mismatches 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 544; DB 2;
Pred. No. 4.7e-35;
                                                                                                  A;Accession: T41325
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                               A; Experimental source: strain 972h-; cosmid c330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31.3%; Score 544; 39.0%; Pred. No. 4
                                                                                                                                                                                                                                                                                                                                A; Map position: 3
C; Superfamily: threonine dehydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: PA2683
C;Superfamily: threonine dehydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 KN--VCIVLSGGNVDL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   || : |::||||||:
KNKRIGIIISGGNVDI 314
                                                                                                                                                                                                                                                                                               A; Gene: SPCC320.14; SPCC330.15c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 122; Conserv
                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-323 <GWI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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                                                                                                                                                                                                                                                                             C; Genetics:
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Matches
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threonine ammonia-lyase (EC 4.3.1.19) YKL218c [similarity] - yeast (Saccharomyces cerevi
N;Alternate names: protein D326
C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:228218; NID:9486390; PIDN:ÇAA82063.1; PID:9486391; MIPS:YKL218d
A;Experimental source: strain 5288C
R;Tzermia, M.; Horaitis, O.; Alexandraki, D.
                                                                                                                                                                                                                                                                                                                                                                                                             Yeast 10, 663-679, 1994

A;Title: The complete sequencing of a 24.6 kb segment of yeast chromosome XI identified edehydratases, membrane transporters, hydantoinases and the phospholipase A(2)-activatia A;Reference number: $44319; MUID:95028164; PMID:7941750

A;Accession: $44320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   threonine ammonia-lyase (EC 4.3.1.19) SPCC320.14 [similarity] – fission yeast (Schizosac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Map position: 11L
C:Superfamily: threonine dehydratase
C:Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: unn.
A;Residues: 1-323 <WOO.
A;Cross-references: EMBL:AL022245; PIDN:CAA18316.1; GSPDB:GN00068; SPDB:SPCC320.14
A;Experimental source: strain 972h-; cosmid c320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247 NTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---SDEKRSKGVIAFSSGNHAQAIALSAKLLNVPATIVMPEDAPALKVAATAGYGAHIIR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 SFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T41297; T41325
R; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Wambutt, R.; Wedler, A; Submitted to the EMBL Data Library, March 1998
A; Reference number: Z21986
                                                              C;Species: Saccharomyces cerevisiae
C;Date: 03 May-1994 #sequence_revision 03 May-1994 #text_change 21-Jun-2002.
C;Accession: S38061; S44320
R;Alexandraki, D.; Tzermia, M.
submitted to the Protein Sequence Database, March 1994
A;Reference number: S38054
A;Reference number: S38054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-226 -rrs>
A;Cross-references: EMBL:X75951; NID:g473130; PIDN:CAA53555.1; PID:g473132
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSS-IGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.7%; Score 587; DB 2; L
illarity 40.9%; Pred. No. 2e-38;
Conservative 66; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  307 NVCIVLSGGNVDL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 128; Conserv
                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-326 <ALE>
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A;Residues: 1401 CARN>
A;Cross-references: GB:AE001716; GB:AE000512; NID:g4980853; PIDN:AAD35443.1; PID:g498
A;Experimental source: strain MSB8
C;Genetics:
                                                                                           threonine ammonia-lyase (EC 4.3.1.19) SCF43A.11C (similarity) - Streptomyces coelicol Cispecies: Streptomyces coelicolor Cispecies: Streptomyces coelicolor Cispecies: Gtreptomyces coelicolor 3.5 Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jun-2002 CiAccession: T36434
Riseager, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, July 1999
A; Reference number: 221598
A; Residues: 1-325 <SEE>
A; Residues: 1-325 <SEE>
A; Resperimental source: strain A3(2)
C; Genetics: 221598
C; Genetics: 221598
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C; Species: Thermotoga maritima
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jun-2002
C; Accession: D72386
R; Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome A;Reference number: A72200; MUID:99287316; PMID:10360571 A;Accession: D72386 A;Status: preliminary
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C;Superfamily: threonine dehydratase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LIPDIPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGWVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADG-VKSSIG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEV 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 YCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.5%; Score 530; DB 2; L
39.3%; Pred. No. 6e-34;
:ive 54; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: SCOEDB:SCF43A.11c
C;Superfamily: threonine dehydratase
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RRVGVILSGGNVD 313
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Matches 123; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C.M.
Nature 399, 323-329, 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        threonine ammonia-lyase (EC 4.3.1.19) [similarity] - Staphylococcus aureus (strain N315) C.Species: Staphylococcus aureus (c)Species: Staphylococcus aureus (c)Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 02-Aug-2002 C;Accession: F89921 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc ma, A.; Maizutan-Iui, Y.; Kobayashi, I.; Cayana, T.; Maizutan-Iui, Y.; Kobayashi, I.; Mayashi, H.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: F89921
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1.346 < CMR>
A; Cross-references: GB: BA000018; PID: g13701236; PIDN: BAB42531.1; GSPDB: GN00149
A; Experimental source: strain N315
C; Genetics:
A; Gene: SA1271
C; Superfamily: threonine dehydratase
C; Keywords: ammonia-lyase; carbon-nitrogen lyase
                                                                         123 YDRYTEDREQIGRDLAQRHGLTLIPPYDHPDVLAGGGTAAKELFEEVGPLDAFFAPLGGG 182
                                                                                                                                                                                                                                           GWVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSS-IGL 246
                                                                                                                                                                                                                                                                       247 NTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVK 306
                                                                                                                                                                                                                                                                                                                                                                       IRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 CDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGG 187
                                                IPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 TYDDVIAAAARIAGHANRTPVMSSRTLDEELGAEVFFKCENLQRMGAFKFRGAFNALSRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 YCISFADVEKAHINIQDSIHLTPVLTSSILNQ-IAGRNLFFKCELFQKTGSFKIRGALNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEGKNVVALVSGGNVDLTRVSGV 330
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C; Species: Agrobacterium tunefaciens
C; Date: 11-3n-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
C; Accession: AF2912
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCl
R; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable threonine dehydratase [imported] - Sinorhizobium meliloti (strain 1021) maga C;Species: Sinorhizobium meliloti
C;Date: 24-Aug_2001 #sequence_revision 24-Aug-2001 #text_change 27-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: F95390 ... Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hubler, F.; B R:Barnett, M.J.; Fisher, R.F.; Jones, T.; Komp, C.; Surzycki, R.; Wells, D.H.; Yeh, K P. Kalman, S.; Keating, D.H.; Palm, C.; Peck, M.C.; Surzycki, R.; Wells, D.H.; Yeh, K P. Kalman, S.; Keating, D.H.; Palm, S. B. 983-9883, 2001 ... A;Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium meli A;Reference number: A95262; MUID:21396509; PMID:11481432
                                                                                                                                                                                                                                                                                                                                                                                                                                          ster, E.W.
A.Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A.Reference number: AB2577; PMID:11743193
A.Accession: AF2912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:AE008688; PIDN:AAL43716.1; PID:g17741247; GSPDB:GN00186 A;Experimental source: strain C58 (Dupont) C;Genetics:
         186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 GGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADG-VKSSIG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 LNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 VEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFOKTGSFKIRGALNAIRGLIPDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 520.5; DB 2;
; Pred. No. 3.3e-33;
44; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: circular chromosome C; Superfamily: threonine dehydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 29.9%;
Best Local Similarity 40.6%;
Matches 127; Conservative 44
                                                                         306 KNVCIVLSGGNVD 318
                                                                                                                    300 ETVIAVASGGNVD 312
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A;Molecule type: DNA
A;Residues: 1-324 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rigodoer, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Woldlam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2333-2338, 2001.
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A;Reference number: A97359; PMID:11743194
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable serine/threonine dehydratase, degradative (PA2683) [imported] - Agrobacterium C; Specids: Agrobacterium tumefaciens (1916: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002 C; Accession: A97687
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A; Residues: 1-324 < KUR>
A; Cross-references: GB:AE007869; PIDN:AAK88450.1; PID:g15157951; GSPDB:GN00169
C; Genetics:
A; Gene: AGR C_4956
A; Map position: circular chromosome
C; Superfamily: threonine dehydratase
                                                                                                                                                                                                                                 LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV 126
                                                                                                                                                                                                                                                        127 YCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 PEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDPS 131
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                                                                                                                                                                   7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRG
                                                                                                                                                                                                                                                                                                                                                  GGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SSIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Gaps
F;51/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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                                                                                            Indels
                                             30.0%; Score 522.5; DB 2;
Similarity 35.8%; Pred. No. 3.1e-33;
14; Conservative 72; Mismatches 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Sim
Matches 114;
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                                                 Query Match
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hypothetical protein tdcB [imported] - Sulfolobus solfataricus C; Species: Sulfolobus solfataricus C; Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Jun-2002 C; Accession: D90166 C; Accession: D9016 C; Accession: D901
                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-405 <KUR>
A;Cross-references: GB:AE006641; NID:913813385; PIDN:AAK40587.1; GSPDB:GN00155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63 LSL---KEEEKKNGVIAVSAGNHAQGVAYAASTLNIKSTIVMPETAPASKYLATKSYGAE 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 IVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQV-PLVDALVVP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGAS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1V-YCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVP 183
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                                                                                                                                                                                                                                                                                            65 RGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGAS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VK-SSIGLNTWPIIRD-LVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 VGGGGLASSVAFLIGNLRPDIEVYLVQPA-----QKELSNFLENGIKCPVDTLDTIADG 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 YLEYFDRIRLAKEKIEKYVHITPIDYSTTFSRIINAKVYLKLENLQKTGSFKVRGAFNKL
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                                                                                                                                                                                VGGGGWVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPP----ETIADG
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                                                                                                                            7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGR--NLFFKCELFQKTGSFKIRGALNAI
        Pred. No. 3.3e-32;
; Mismatches 115;
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----PAHIKRPLVILCGGNVD 311
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    37.78;
            Best Local Similarity 37.7
Matches 121; Conservative
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Matches 126; Conserv
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A; Status: preliminary
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                                                                                                                                                      A:Coss-references: GB:AE006469; PIDN:AAK65688.1; PID:g14524179; GSPDB:GN00165
A:Experimental source: strain 1021, megaplasmid pSymA
A:Experimental source: strain 1021, megaplasmid pSymA
GGalibert, F:: Finan, T. F.; Publer, Pela, D:: Chain, P:: Cowie, A:: Davis, R.W.; Dreano, S:: Federspiel, N.A.; Fisher, R.F.;
L.; Hyman, R.W.; Jones, T.
A:Authors: Kahn, D:: Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, Hebault, P:: Vandenbol, M.: Vorholter, F.J.; Weidner, S:: Wells, D.H.; Wong, K.; Yeh, K. A:Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A:Contents: annotation
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   phos
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C; Accession: T24337
C; Lennard, N.
Submitted to the EMBL Data Library, September 1996
A; Reference number: 219877
A; Status; preliminary; translated from GB/EMBL/DDBJ
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Gross-references: EMBL: Z80219; PIDN: CAB02298.1; GSPDB: GN00019; CESP: T01H8.2
A; Construction of C; Genetics: A; Genet
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A:Introns: 75/3; 131/2; 159/3; 203/1; 259/3; 276/3
C:Superfamily: threonine dehydratase
C:Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase;
F:56/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 TPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDP 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSSI-GLNTW
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C;Superfamily: threonine dehydratase
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Matches 118; Conservative
A; Accession: F95390
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-323 <KUR>
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12;

Length 405;

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threonine ammonia-lyase (EC 4.3.1.19) [similarity] - Salmonella enterica subsp. enter C; Species: Salmonella enterica subsp. enterica serovar Typhi
A: Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 02-Aug-2002
C;Accession: AB0897
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr Noule, S.; O'Gaorra, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A.Thitle: Complete genome sequence of a multiple drug resistant Salmonella enterica se A;Reference number: AB0502; PMID:11677608
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                                                                                                                                                                                                                                                                                       LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV 126
                                                                                                                                                                                                                                                                                                                                                                                                                     204 IHGADYDDAQAHAHE-----EAAEGRTYVHAFDDEYIMAGQGTLGLEIAADCPTVDTV 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 K-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQ 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB: AL513382; PIDN: CAD07768.1; PID: 916504317; GSPDB: GN00176
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                                                                                                                                                                                                                                                                                                                                   LSAD ---QODAGVVTASAGNHAQGVALAASRSGVDSKVVMPESAPISKIKATKSYGAEVV
                                                                                                                                                                                                                                                                                                                                                                                        ----YCDPSDESREKVTQRIMQETEG-ILVHPNQEPAVIAGQGTIALEVLNQVPLVDAL
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                                                                                                                                 19;
                                                                               Length 495;
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                                                                                                                                   Indels
                                                                               5;
                                                                            Score 492.5; DB 2
Pred. No. 9.1e-31;
9; Mismatches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 28.2%; Score 491; DB 2; Best Local Similarity 36.8%; Pred. No. 6.9e-31; Matches 121; Conservative 68; Mismatches 116,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Keywords: ammonia-lyase; carbon-nitrogen lyase
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                                                                                                                                 59;
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C; Superfamily: threonine dehydratase
                                                                               28.3%;
36.5%;
                                                                                                                                 Conservative
                                                                                                      Best Local Similarity
Matches 119; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 1-329 <PAR>
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                                                                               Query Match
                          iluA
     C; Genetics
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                                                                                                                                                                     threonine dehydratase [imported] - Caulobacter crescentus
Cispecies: Calopar-2001 #sequence_revision 20-Apr-2001 #text_change 31-Dec-2001
Ciscoration: G87633
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon n., J.; Ermolaeva, M.; White, O.; Salzbary, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173698; PMID:11259647
A:Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C.Accession: H88359
R.NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, J. Leithauser, B.; Reiller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl. Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A.Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; L. A; Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecule type: DNA_
Residues: 1-325 <STO>
Cross-references: GB:AE005673; NID:g13424763; PIDN:AAK25067.1; GSPDB:GN00148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 PVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKS 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : | : : | | : : | | : | 100 FYDRFTEDRVAIADQIAAERGCVVVPSYDDPHIIAGQGTVGLEIVAQAAAQGATLDRLIC 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQV----PLVDALVV 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 CVGGGGLIAGTSTAVKALSPATEIWGVEPAGFDETRRSLESGRRETIDKDARSICDALLT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 SI-GLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: GB: AE004437; NID: 910581515; PIDN: AAG20244.1; GSPDB: GN00138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRG 66
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Pred. No. 1.7e-31;
58; Mismatches 133;
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NGIDKKVISLVSGGNIDLSLLS 315
SPEVKNVCIVLSGGNVDLTSLN 323
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C,Superfamily: threonine dehydratase
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Best Local Similarity 36.3%
Matches 115; Conservative
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A;Molecule type: DNA
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302
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C; Genetics
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RESULT 1
                                                                                     June 24, 2003, 05:44:58; Search time 41.4389 Seconds (without alignments) 1685.614 Million cell updates/sec
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1740
1 MCAQYCISFADVEKAHINIQ.....TSLNWVGQAERPAPYQTVSV 339
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                      671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_human:*
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sp_bacteriap:*
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sp_phage:*
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Maximum DB seq length: 200000000
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sp_bacteria:*
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sp_rodent:*
sp_virus:*
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                                                                                                                                                                               Sequence:
                                                                                                                                                                                                                                                      Searched:
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                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES

Q9tOdl arabidopsis Q8xpXO ralstonia s Q8xQ10 neurospora Q910f5 pseudomonas Q99u50 staphylococ Q9xaa4 streptomyce Q9wyjl thermotoga Q8ubw5 agrobacteri Q92y58 rhizobium m Q93968 caenorhabdi Q975y3 sulfolobus Q8x177 clostridium Q930pl sulfolobus Q93177 clostridium Q930pl sulfolobus Q93177 clostridium Q930pl sulfolobus Q93174 caulobacteri Q94nh6 halobacteri Q8x3X4 salmonella Description 09T0D1 08XPX0 08X0J0 0910F5 099U50 Q9WYJ1 Q8UBW5 Q92Y58 Q93968 Q975Y3 Q9A3U7 Q9HNH6 Q8Z3K4 Q8XL77 Q980P1 Query Match Length DB 317 404 405 405 325 329 Score 791 620 534 534 535 530 530 522.5 522.5 507.5 501 501 499 498.5 Result 80.

Q8rdt9 fusobacteri Q9ewg3 streptomyce Q97cb2 thermoplasm Q9hlw2 thermoplasm Q829v3 yersinia pe		O9Pp95 campylobact O92d93 rickettsia O9rwu8 deinococcus O98f73 rhizobium 1	0.0	C)	O9ybvl aeropyrum p Q8zab4 yersinia pe Q9kvwl vibrio chol Q9auq1 oryza sativ Q8w314 oryza sativ Q8z378 salmonella
Q8RDT9 Q9EWG3 Q97CB2 Q9HLW2 Q8Z9V3	Q92HZ2 Q8ZVF0 Q916G0 Q9VHF0	Q9PP95 Q92D93 Q9RWU8 Q987A3	Q9AZDU Q98DQ4 Q8U6P8 Q95XY8 Q21080	Q985M4 Q92WC4 O94634 P73375 Q91418	Q9YBV1 Q8ZAB4 Q9KVW1 Q9AUQ1 Q8W314 Q8Z378
16 16 17 17 16	16 17 16 5	16		16 16 16	17 16 10 10
404 409 406 406 320	343 403 504 469	333 352 352	327 336 448 512	334 334 600 515	349 514 510 602 602 514
28.0 27.8 27.0 26.9 26.9	26.8 26.7 26.6 26.0	25.5 25.5 25.4 25.3	24.52	23.7 23.8 23.7 23.5	22.3 22.9 22.3 22.3 22.3
487 483.5 470 468	466.5 464 463.5 453	446.5 444.5 441.5 440.5	4 2 3 3 4 4 2 4 4 2 3 4 4 2 4 4 2 4 4 2 4 4 4 2 4 4 4 4	419 414 413 409.5 406.5	398 398 388 5 388 5
	223	23 23 23 23 23 23 23 23 23 23 23 23 23 2	333	33 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	0 H 4 4 4 4 4 5
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ALIGNMENTS

1 0970D1 PRELIMINARY; PRT; 346 AA. 0970D1 01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 175C23.70 Protein. 17

a

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YCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGG 186
                                                                                                                                      ||:::|| :|||:::|
183 GCLLSGCATAARALSPACRIIGVEPPAGNDGQQSLRKGEIV-HIDTPATIADGAQTQHLG 241
                                                                                  123 FYDRYTEDREAIGRRLAEQHGLTLIPPYDHPHVMAGQGTAAKELIEETGPLDLLLVCLGG 182
                                                                                                                                                                               246 LNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEV 305
                                                                                                                                                                                                253 PILVPGAEPSFSGADDGRRGYSGTRIESVKSL----TIADGLRTPLGAYPWSIIYERKL 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 TAALELORQVAASLSTSGTTTTNRRRLNAIITPCGGGGLLSGTALACSDLSPSDPSTPG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        256 VDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALA-AVLSQHFQTV----SPEVKNVC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 ELFQKTGSFKIRGALNAIRGLIPDTPEE--KPKAVVTHSSGNHGQALTYAAKLEGIPAYI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              105 VVPQTAPNCKKLAIQAYGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204 -VKVYAAEP--SNADD----CYQSKLKGELTPNLHPPETIADGVKSSIGLNTWPII--RDL.
                                                                                                                 GGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSS-IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 TIALEVLNQVPL------VDALVVPVGGGGWVAGIAITIKALKPS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Holland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neurospora crassa.
Eukaryota; Fungi, Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoheisel J., Brandt P., Fartmann B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 ADVEKAHINIQDSIHLTPVLTSSILNQIAGR-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         German Neurospora genome project;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AL670005; CAD21283.1;
InterPro; IPR001926; B6_enzyme_beta.
Pfam; PF00291; PALP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B. Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41505 MW; 02BFB864B95716A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.4%; Score 546; DB 3; 37.5%; Pred. No. 2.9e-35;
                                                                                                                                                                                                                                                                                                                                                               ΑA
                                                                                                                                                                                                                                                                                                                                                            388
                                                                                                                                                                                                                                                                | | :::|||||||
| KRVGVIISGGNVDLQHFARLVQAD 322
                                                                                                                                                                                                                                               KNVCIVLSGGNVDLTSLNWVGQAE 329.
                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Creat
01-MAR-2002 (TrEMBLrel. 20, Last
01-JUN-2002 (TrEMBLrel. 21, Last
Related to threonine dehydratase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 140; Conservative
                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 388 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                99
                                                                                                                                                                                                                                                                                                                                                                                            243 TLPVTNTIADGLRASLGDLTWPVVRDLVDDVVTLEECEIIEAMKMCYEILKVSVEPSGAI
                                                                                                                                  TAPNCKKLAIQAYGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIAL
                                                                                                                                                                                                                                                                                                          EVLNQVPLVDALVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --KTGSFKIRGALNAIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQ
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arliguenave F., Gouzy J., Mangenot S., Chalat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chandler M., Choisne N., Claudel-Fenard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Meissenbach J., Boucher C.A.; "Genome sequence of the plant pathogen Ralstonia solanacearum."; Nature 415:497-502(2002).

EMBL, AL646085, CAD18667.1; -
InterPro; IPR01926; B6_enzyme_beta.

Pfam; PF00221; PALD; I.
                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.6%; Score 620; DB 16; Length 323; 41.0%; Pred. No. 2.9e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                              4 QYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQ
                                                   Length
Hypothetical protein.
SEQUENCE 346 AA; 36839 MW; 47C37E1CA52B91F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34515 MW; 2175CBF693E04A2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable amino-acid dehydratase protein (EC 4.2.--).
RSP1516 OR RSO4793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLAAVLSNSFRN-NPSCRDCKNIGIVLSGGNVDLGSL-W 339
                                                                                                                                                                                                                                                                                                                                                                                                                                        ALAAVLSQHFQTVSP---EVKNVCIVLSGGNVDLTSLNW 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ralstonia solanacearum (Pseudomonas solanacearum).
Plasmid megaplasmid.
                                             .5%; Score 791; DB 10;
.9%; Pred. No. 7.9e-55;
e 68; Mismatches 88;
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MEDLINE-21681879; PubMed=11823852;
                                             45.5%;
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es 133; Conserv
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                                                                              Matches 159;
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                                              Query Match
Best Local 3
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Q8XPX0;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           247 NTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              309 VAGMYSVGEEEIKKALRLVYERMKVVVEPSAVVGLAVALFNEEFRSMVEREGGEEGWDLG 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 CDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68 IPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 SFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGL 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=ATCC 15692 / PAO1;
MEDIINE=20437337; PubMed=10984043;
MEDIINE=20437337; PubMed=10984043;
Stover C.K., Pham P. S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Hickey M.J., Brinkman P.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
Pseudomonas.
NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.3%; Score 544; DB 16; Length 320; 39.0%; Pred. No. 3.2e-35; ive 62; Mismatches 121; Indels 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           320 AA; 33957 MW; C6F97C6259FE8584 CRC64;
                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable serine/threonine dehydratase, degradative.
                                                                                                                                                                                                      320 AA
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                                                                                                                                                                                                   PRT;
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                                          310 IVLSGGNVDLTSL 322
                                                                :| ||||||:| :|
369 VVFSGGNVELAAL 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               307 NVCIVLSGGNVDL 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               opportunistic pathogen."
Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                         PA2683.
Pseudomonas aeruginosa
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64 IRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGA 123
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                                                                                                                                                                                                                                                                                                                                                                    SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
MEDLINE-2131952; PubMed=11418146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-O., Ito T.,
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K., Yoshino C., Shiba T.,
"Whole genome sequencing of meticillin-resistant Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 VGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSS
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                                                                                                                                                                                    Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
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                                                                                                                                                          Staphylococcus aureus (strain Mu50 / ATCC 700699), and
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative threonine dehydratase.
SCO0821 OR SCF43A.11C.
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
SA1271 protein (Threonine deaminase IlvA homolog).
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TIGREAMS; TIGR01127; ilva_lcterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
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InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
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EMBL; AP003362; BAB57600.1; -.
EMBL; AP003133; BAB42531.1; -.
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Matches 122; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A set of ordered cosmids and a detailed genetic and physical map for the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Kieser H.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2).";
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James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-1999) to the EMBL/GenBank/DpBJ databases
                                                                                                                                                             Seeger K., Harris D.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
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InterPro; IPR000634; S/T_dehydrtse.
Pfam: PF00291; PALP; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
SEQUENCE 325 AA; 33965 WW; 4E1DE62D340489A7 CRC64;
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39.3%; Pred. No. 4.2e-34;
ive 54; Mismatches 128;
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MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 417:141-147(2002).
EMBL; AL096837; CAB48898.1; -.
HSSP; P04968; 1TDJ.
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Matches 123; Conservative
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                SEQUENCE FROM N.A.
                                                                  NCBI_TaxID-1902;
                                                                                                                                        STRAIN=A3(2);
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LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV 126
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                                                                                                                                                                                                                                                                                                    MEDLINE=99287316; PubMed=10360571;
MEDLINE=99287316; PubMed=10360571;
Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
Haft D.H., Hickey E.K., Malek J.D., Nelson W.C., Ketchum K.A.,
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Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  187 GCMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SSIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                   Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
NCBL_TaxID=2336;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43110 MW; 4D757A8F83786180 CRC64;
                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Threonine dehydratase catabolic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 522.5; DB 1
Pred. No. 2.3e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30 0%; Sco. 35.8%; Pred. No. 4...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA
  ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF01842; ACT; 1.
Pfam; PF01842; ACT; 1.
Pfam; PF00291; PALP; 1.
TIGRPAMS; TIGR01127; ilvA_ICterm; 1.
Complete proteome.
SEQUENCE 401 AA; 43110 MW; 4D757A8F83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       324
401
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InterPro, IPR001926; B6_enzyme_beta.
InterPro, IPR000634; S/T_dehydrtse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KNVCIVLSGGNVDLTSLN 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE001716; AAD35443.1; -. HSSP; P04968; 1TDJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                Thermotoga maritima.
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                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8UBW5
Q8UBW5;
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GGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADG-VKSSIG 245.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQ-----VPLVDALVVPVGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEDRDAIGNRLSSERGLTLIRPYDEPLVIAGOGTAGLEIAEOGAELGIGAAEVL-VPCGG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 LNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21608551; PubMed=11743194; MEDLINE-21608551; PubMed=11743194; MEDLINE-21608551; PubMed=11743194; Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Holmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Holmagan C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Stater S., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S., Geneme sequence of the plant pathogen and biotechnology agent Agrobacterium tumefaciens CSB.", Science 294:2323-2328(2001).
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Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chan Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
Chapwan P., Clandenning J., Daatherage G., Gillet W., Grant C.,
Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       The genome of the natural genetic engineer Agrobacterium tumefaciens
                                                                              ILVA OR ATU2735 OR AGR_C_4956.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
NCBI_TaxID=176299;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29.9%; Score 520.5; DB 16; Length 40.6%; Pred. No. 2.4e-33; Live 44; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 AA; 33726 MW; B2000A00488F7C1C CRC64;
    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                      SEQUENCE FROM N.A. MEDLINE=21608550; Pubmed=11743193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE009221; AAL43716.1; -. EMBL; AE008187; AAK88450.1; -.
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ETVIAVASGGNVD 312
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                                                                Threonine dehydratase
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Best Local Similarity
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RESULT 9 Q92Y58

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TPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIVYCDP 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMV 190
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Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
Sinorhizobium mellioti pSymA megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
EMBL, AE007289; AAK65688.1;
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR00194; S/T_dehydrtse.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 AGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVKSSI-GLNTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                          Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Sinorhizobium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29.7%; Score 517.5; DB 16; Length 323; 37.7%; Pred. No. 4.2e-33; ive 60; Mismatches 128; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative threonine dehydratase.
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Last annotation update)
   323 AA
                                                                                                          Rhizobium meliloti (Sinorhizobium meliloti)
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    PRT;
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                                                                                                                          Plasmid pSymA (megaplasmid 1)
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02,
21,
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Matches 118; Conservative
PRELIMINARY;
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Caenorhabditis elegans.
                                                                                           RA1030 OR SMA1872
                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                       NCBI_TaxID=382;
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STRAIN=13
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Q8XL77
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                                                                                                                                                                                                                                                                                                                                                                                        VGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPP----ETIADG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                      RGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGAS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VK-SSIGLNTWPIIRD-LVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |: :| ||: | | |: 235 VRVARVGPLCEPILKQYCAQKVISVKEDEIKEGIKLIWTRWKQRIEPTAALAFAGVLYHK 294
                                                                                                                                                                                                                                                                                              7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGR--NLFFKCELFQKTGSFKIRGALNAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M., Sekine M., Baba S.-T., Ankai A., Kosuqi H., Hosoyama A., Fukui S., Nagai Y., Nishlijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y., Yoshizawa T., Takamiya M., Kato Y., Kudoh Y., Yamazaki J., Kushida M., Oguchi A., Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamägishi A., Coshima T., Kikuchi H.;
                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                            23;
                                                                                                                                                                                                                                   29.2%; Score 507.5; DB 5; Length 317; 37.7%; Pred. No. 2.5e-32; ive 62; Mismatches 115; Indels 23.
                                                                                                       Genome sequence of the nematode C.elegans: A platform for
                                           Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                             InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
Pfam. PF00291; PALP; 1.
PROSITE; PS00165; DEHYDRATSE_SER_THR; 1.
SEQUENCE 317 AA; 34688 WW; 0F0DE6C7479389E3 CRC64;
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last sequ
01-JUN-2002 (TrEMBLrel. 21, Last anno
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----PAHIKRPLVILCGGNVD 311
                                                                     SEQUENCE FROM N.A.
MEDLINE~99069613; PubMed=9851916;
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                                                                                                                  investigating biology.";
Science 282:2012-2018(1998).
EMBL; 280219; CAB02298.1; --
HSSP; P35520; 1JBQ.
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STRAIN=JCM 10545 '/ 7;
PubMed=11572479;
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NCBI_TaxID=111955;
                     SEQUENCE FROM N.A.
NCBI_TaxID=6239;
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Shinizu T., Ohtenin K., Hirakawa H., Ohshima K., Yamashita A.,
Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
"Complete genome sequence of Clostridium perfringens, an anaerobic
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Bacteria; Firmicutes, Bacillus/Clostridium group, Clostridia;
Clostridiales; Clostridiaceae, Clostridium.
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Hypothetical protein; Complete proteome.
SEQUENCE 404 Aa; 44034 MW; 4C4B44D776FE26B7 CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP003189; BAB80871.1;
InterPro: IPR002912; AcT.
InterPro: IPR001926; B6_enzyme_beta.
InterPro: IPR000634; S/T_dehydrtse.
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Pred. No. 1.2e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                         28.9%; Score 502.5; DB 1738.9%; Pred. No. 8.9e-32;
Crenarchaeon, Sulfolobus tokodaii strain7.";
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Pfam; PF000291; PALP; 11.
TIGREAMS; TIGR01127; ilva lCterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
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                                             DNA Res. 8:123-140(2001).
EMBL; AP000982; BAB65265.1;
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67 LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV 126
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                                                                                                                                                                                                                                                  SSIGENTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTV 301
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STRAIN-ATCC 19089 / CB15;
MEDLINE-21173698; Dubmed-11259647;
MEDLINE-21173698; Dubmed-11259647;
MICHMAN W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Elsen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B., DeBOY R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shappiro L., Fraser C.M.;
Complete genome sequence of Caulobacter crescentus.";
Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
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                                                    IV-YCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVP
                                                                                                                                                    VGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADG--VK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E71D0AC7033115E4 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.6%; Score 498.5; DB 10 36.3%; Pred. No. 1.4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 AA
                                                                                                                                                                                                                                                                                                                                                                                  294 NGIDKKVISLVSGGNIDLSLLS 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B6_enzyme_beta
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17,
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Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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01-JUN-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caulobacter crescentus
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Pfam; PF00291; PALP;
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Best Local S
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                                                                                                                                                  EKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASI-----VYC 128
                                                                                                                                                                              DPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGG 188
                                                                                                                                                                                                                                                                               189 MVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGVK-SSIGLN 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVSPEVKN 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 RGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGAS 124
                                              KAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRGLIPDTPE 73
                                                                           5 YCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAI 64
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LISGVILAAKALNPNVKVIGVQAEGANAMVKSFKAGEIIA-LDAVDTIADGIAVKRPGDL
  Gaps
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Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
  20;
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60; Mismatches 124; Indels
  Indels
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Threonine dehydratase catabolic (threonine deaminase)
Mismatches 112;
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InterPro; IPR002912; ACT.
InterPro; IPR001926; B6_enzyme_beta.
Pfam; PF00842; ACT; 1.
Pfam; PF00291; PALP; 1.
TIGRFAMS; TIGR01127; ilva_lCterm; 1.
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STRAIN-ATCC 35092 / DSM 1617 / P2;
MEDLINE-21332296; Pubmed=11427726;
67;
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297 IVSVISGGNIDMVTI 311
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Conservative
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116;
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Matches 12
Matches
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240 PIPGDLTWPINQKNLSGVVAVTDAEVAEAMRYAFSTLKLVVEPGGCVALTAALTGKVDVA 299
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NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,

Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,

Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,

Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,

Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,

Isenbarger T.A., Peck R.F.; Pohlschroder M., Spudich J.L., Jung K.-H.,

Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,

Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;

Genome sequence of Halobacterium species NRC-1.",

Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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Archaea; Buryarchaeota; Halobacteria; Halobacteriaceae;
Halobacteriaceae; Halobacterium.
NCBL_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Threonine dehydratase.
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PROSITE; PS00165; DEHYDRATASE_SER_THR; UNKNOWN_1.
COMDLETE proteome.
SEQUENCE 495 AA; 53095 MW; 8F203680AAF93F80 CJ
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InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR0010926; S/T_dehydrtse.
Pfan; PF001842; ACT; 1.
Pfan; PF00291; PALP; 1.
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                                                                                                                                     302 SPEVKNVCIVLSGGNVD 318
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Mutant

Title: Perfect score:

Sequence:

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Scoring table:

Searched:

Minimum DB seq Maximum DB seq

Database

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Serine racemase; N-methyl-D-aspartate receptor; neural death; neural dysfunction; NMDA receptor; Parkinson's disease; Huntington's disease; motor neurone disease; Alzheimer's dise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of a murine serine racemase polypeptide
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21-JUL-1999;
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983.448 Million cell updates/sec
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                             908470 seqs, 133250620 residues
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Maximum Match 1008
Listing first 45 summaries
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1 MCAQYCISFADVEKAHINIQ.
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Threonine dehydrat Threonine dehydrat Threonine dehydrat Threonine dehydrat

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Novel human enzyme

's disease

Mothet J, Brady RO;

Snyder SH, Wolosker H, Sheth K, Masaaki T,

1740

1582.5 1582.5 1582.5 1582.5 1578.5 1574.5

453 435.5

Score

Result 80. Brady

Mothet J,

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The present sequence represents a mammalian serine racemase, which has a specific activity of at least 0.003 micromole L-serine/mg/hour. The enzyme catalyyses the direct racemisation of L-serine to D-serine. D-serine appears to be an endogenous ligand of N-methyl-D-aspartate (NMDA) receptors. The mammalian serine racemases can be used to identify modulators, which can be used in the treatment of acute or chronic neural death or dysfunction mediated by overactivation of N-methyl-D-aspartate (NMDA) receptors. Overactivation of the receptors is associated with Parkinson's disease, Huntington's disease, motor neurone
                                                                                                                                                                                                                                                                                                   which can be used to treat diseases associated with N-methyl-D-aspartate receptor overactivation, e.g. Alzheimer's disease
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                                                                                                                                                                                                                                                                                 Mammalian serine racemase preparations, used to identify modulators
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89.7%; Pred. No. 3.7e-153;
iive 19; Mismatches 15;
                                                                                                                                                                  Wolosker H, Sheth K, Masaaki T,
                                                                                                                              (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 50-51; 54pp; English.
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               18-JAN-2000; 2000WO-US00938
                                                    99US-0116333
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Matches 305; Conserv
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                                                    19-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LNAIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a mammalian serine racemase, which has a specific activity of at least 0.003 micromole L-serine/mg/hour. The enzyme catalyses the direct racemisation of L-serine to D-serine. D-serine appears to be an endogenous ligand of N-methyl-D-aspartate (NMDA) receptors. The mammalian serine racemases can be used to identify nedulators, which can be used in the treatment of acute or chronic neural death or dysfunction mediated by overactivation of N-methyl-D-aspartate (NMDA) receptors. Overactivation of the receptors is associated with Parkinson's disease, Huntington's disease, motor neurone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                    Mammalian serine racemase preparations, used to identify modulators which can be used to treat diseases associated with N-methyl-D-aspartate receptor overactivation, e.g. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MCAQYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of a human serine racemase polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSPEVKNVCIVLSGGNVDLTSLNWVGQAERPAPYQTVSV 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1740; DB 21;
Pred. No. 2.7e-169;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7; Page 48-49; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB07734 standard; Protein; 340
                                                                                                                                                                                                                                                                                                                                                                                           disease and Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ·
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
100.0%;
                                                N-PSDB; AAA59294, AAA59300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 100.
Matches 339; Conservative
                             2000-482915/42
                                                                                                                                                                                                                                                                                                                                                                                                                              339 AA;
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neural dysfunctio
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Sequence

Claim

Query Match

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181 241

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301

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301

AAB0773

Gaps

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Indels

Length 340;

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anxiety; glaucoma; stroke; hyperalgesia; pain; spinocerebellar ataxia; schizophrenia; transgenic animal; chromosome 17p13; immunogen.
serine racemase; Parkinson's disease; Huntingdon's disease;
     Human;
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Homo sapiens

WO200175144-A1

11-0CT-2001

02-APR-2001; 2001WO-US10662.

04-APR-2000; 2000US-194451P

(MERI) MERCK & CO INC.

Connolly T, Liu Y,

2001-656991/75 N-PSDB; AAS15217

identifying compounds that alter enzyme activity (e.g. including compounds that inhibit or stimulate enzyme activity) or in generating antibodies against the protein useful in assays for recombinant serine racemase polypeptide,

Claim 7; Page 14; 43pp; English.

human serine racemase, vectors containing it, host cells expressing the racemase, methods of identifying inhibitors of serine racemase and a tracemase, methods of identifying inhibitors of serine racemase and a transgenic animal lacking a functional endogenous serine racemase comprising the human serine racemase of the invention. The racemase comprising the human serine racemase of the invention. The racemase comprising the human serine racemase of the protein and in structural studies of the protein and structural studies of the protein and structure/function relationships of the protein. Biologically active fromedion and mutant or polymorphic forms of the serine racemase colypeptide have diagnostic, therapeutic or prophylactic uses (e.g. carvicty, glaucoma, strucke, hyperalgesia, pain, spinocerebellar ataxia and schizophrenia), and would be useful for sceneing for modulators and/or inhibitors of serine racemase function. The polynucleotides are useful as protein as probes for the specific detection of the presence of a polynucleotide encoding a serine racemase protein. The transgenic animal is useful for the study of the tissue and temporal specific expression or activity of the study of the tissue and temporal specific expression or activity of the strine racemase gene in an animal. The gene for human serine represents human serine

340 AA; Sequence

1; Gaps DB 22; Length 340; Indels Query Match 90.9%; Score 1582.5; DB 22 Best Local Similarity 89.7%; Pred. No. 3.7e-153; Matches 305; Conservative 19; Mismatches 15;

9 1 MCAQYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGA

ò g ò Q ò 음 ò

120 LNAIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQA 61

/label= Casein_kinase_II_phosphorylation_site label = Casein_kinase_II_phosphorylation_site

. 215

Modified-site Modified-site Modified-site

.238

/label= Casein_kinase_II_phosphorylation_site

/label= N_myristoylation_site 308..326

/label- Transmembrane_domain

'label= N_myristoylation_site

264

292

Modified-site

Doma i.n

239..244

- 120 180 YGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDAL 121 61
- 240 VVPVGGGGWVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGV 181

121

/note= "Serine/threonine dehydratases pyridoxal-phosphate 181 VVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGV 240 KSSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQT 300 Human: pyridoxal phosphate dependent enzyme; nootropic; neuroprotective; enticonvulsant; cerbroprotective; cardiant; vasotropic; gene therapy; epilepsy; Alzheimer's disease; chromosome 17; serine racemase; stroke; behavioural change, neurodegenerative disorder; schizophrenia; atresia; rheumatic heart failure; circulatory disorder; hepatic injury; jaundice; lung disorder; nodular hyperplasia; stenosis; skeletal muscle disorder; tumour; rhabdomyosarcoma; dermal fibroblast disorder. /label= Casein_kinase_II_phosphorylation_site 19.315 //note= "Pyridoxal-phosphate dependent enzyme family domain" /note= "cAMP and cGMP-dependent protein kinase //abel= Protein_kinase_C_phosphorylation_site 54..56 /label= Protein_kinase_C_phosphorylation_site /label= Casein_kinase_II_phosphorylation_site /label= Protein_kinase_C_phosphorylation_site /label- Protein_kinase_C_phosphorylation_site Human pyridoxal-phosphate dependent enzyme 22406 protein. VSPEVKNVCIVLSGGNVDLT-SLNWVGQAERPAPYQTVSV 339 59..64 /label= N_myristoylation_site 88..93 N_myristoylation_site /label- N_myristoylation_site /label= Transmembrane_domain phosphorylation site" Location/Qualifiers AA. attachment site" AAE08342 standard; Protein; 340 (first entry) .198 09.112 140..143 187..192 205 /label= Key Modified-site Homo sapiens 15-NOV-2001 AAE08342; 241 241 301 301 Domain Domain AAE08342 RESULT g ò οy g

(first entry)

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Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the .
                                                                            Human; primer; detection; diagnosis; antisense therapy; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; SEQ ID 15149; 2537pp + CD ROM; English.
                                                  Human protein sequence SEQ ID NO:15149.
                                                                                                                                                                                  28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                      (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                     WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                    full-length cDNAs
                                                                                                                                                                                                                                                                                                                Isogai
                                                                                                                                                                                                                      27-AUG-1999;
11-JAN-2000; 2
02-MAY-2000; 2
                                                                                                       Homo sapiens.
                                                                                                                               EP1074617-A2
                                                                                                                                                                                                                                                              09-JUN-2000;
                                                                                                                                                                                                          29-JUL-1999;
                        26-JUN-2001
                                                                                                                                                         07-FEB-2001
AAB94477;
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Dp
                                                                                                                                                                                                                                                                               The present sequence is human pyridoxal phosphate dependent enzyme 22406 which is a serine racemase. Human 22406 gene is located on chromosome 17 between D178349 and D178796. The protein 22406 is a modulator of D-serine. D serine has been shown to modify behavioural changes associated with learning, memory and convulsions. Human 22046 and compounds that modulate the expression or activity are used to treat or diagnose neurodegenerative disorders including Alzheimer's disease, schizophrenia as well as quell anxiety and epilepsy and prevent damage from stroke as well as cardiac (heart failure, rheumatic heart failure) and circulatory disorders, liver disorders (hepatic injury, jaundice), lung disorders, prostrate disorders (benign enlargement, nodular hyperplasia), colon disorders (atresia, stenosis), skeletal muscle disorders (tumours-rhabdomyosarcoma) and dermal fibroblast disorders. Human 22406 cDNA is also useful in gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Gaps
                                                                                                                                                                                                         Novel polypeptide of the human pyridoxal phosphate dependent family useful in screening and detection assays and for treatment, e.g. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90.9%; Score 1582.5; DB 22; Length 340; 89.7%; Pred. No. 3.7e-153;
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19; Mismatches 15;
                                                                                                                                                                                                                                                            Claim 8; Fig 1; 121pp; English.
                                                                                                                (MILL-) MILLENNIUM PHARM INC
                                                             20-FEB-2001; 2001WO-US05365
                                                                                     17-FEB-2000; 2000US-0183208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity 89.7
Matches 305; Conservative
                                                                                                                                                                                                                                    epilepsy and Alzheimer's
                                                                                                                                           Rudolph-Owen
                                                                                                                                                                 WPI; 2001-529909/58
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         WO200160987-A1
                                   23-AUG-2001
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Saito K, Ya Otsuki T;

Hayashi K, S A, Nagai K,

Wakamatsu Nishikawa T,

Sugiyama T,

2000JP-0118776. 2000JP-0183767.

2000JP-0241899

99JP-0300253

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polynucleotide which comprises a 3-april graduate the polynucleotide which comprises a 1-april graduate, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-and sequence/3'-and sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dr primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprision a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
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89.7%; Pred. No. 3.7e
ive 19; Mismatches
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Best Local Similarity 89.7
Matches 305; Conservative
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AAB94477 standard; Protein; 340 AA

AAB94477

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                  KSSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQT 300
                                                                          VVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGV
                                                                                               ynucleotide encoding serine racemase enzyme and the enzyme useful screening reagents regulating the activity of the enzyme in a ron disease caused by over- or under-activation of glutamate
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  attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of human serine racemase, an enzyme that catalyses the conversion of L-serine to D-serine. Neuron damage following various nervous system diseases is often caused by activation of glutamate N-methyl-D-aspartate (NMDA) receptors in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glutamate N-methyl-D-aspartate receptor; neurodegenerative disease; stroke; Alzhainer, s disease; Parkinson's disease; pain; myopathy; nootropic; neuroprotective; cerebroprotective; antiparkinsonian; analgesic; diagnosis; therapy; screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           serine/threonine dehydratase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pyridoxal-phosphate attachment site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         requlation;
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                                                                                                                                                                                                                                                                                                                                                                            AAM50262 standard; Protein; 340 AA.
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/note= "prosite
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03-APR-2000; 2000US-194249P.
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N-PSDB; AAI70575.
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121
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LNAIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the brain. This receptor is activated by the binding of D-serine.

Regulation of D-serine levels through regulation of serine racemase may therefore prevent or minimise neuron damage in neurogenic and may therefore prevent or minimise neurons and respect to the neurons of disease in mer and shall also and chronic pain. The invention provides serine racemase and chronic pain. The invention provides serine racemase polypeptides and methods for their recombinant production. These polypeptides are used in claimed methods of screening for agents that modulate or decrease serine racemase activity. A claimed paramaceutical composition comprising either an expression vector that contains a serine racemase polynucleotide, or a reagent that modulates serine racemase polynucleotide, or a reagent that contains a serine racemase polynucleotide, or a reagent that serine racemase enzyme activity, is used to modulate serine racemase enzyme activity, is used to modulate serine racemase activity in a disease, particularly neuron damage or a neurodegenerative disease caused by the over- or under-activation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MCAQYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MCAQYCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serine/threonine dehydrase 37; cancer; HIV infection; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.7%; Score 1578.5; DB 2
89.4%; Pred. No. 9.4e-153;
tive 20; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG78808 standard; Protein; 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 89.49
Matches 304, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340 AA;
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YGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDAL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
                                                                       Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                  (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MCAQYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGA
                                                                                                                                                                                                                                                                                                                                                                                                              disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaem:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                       Claim 11; SEQ ID NO 2089; 2081pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster polypeptide SEQ ID NO 17916.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 988; DB 23;
Pred. No. 1.5e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VVPVGGGGWVAGIAITIKALKPSVKVYAAEP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Mismatches
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                  2002-122018/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 189; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            228 AA;
                                    N-PSDB; ABL90122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGASIVYCDPSDESREKVTQRIMQETEGILVHPNQEPAVIAGQGTIALEVLNQVPLVDAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibecterial; antifungal; antiperasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                   1 MCAQYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGA 60
                                                                   Polypeptide-serine/threonine dehydrase 37 and polynucleotide for coding this polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                          KSSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETIADGV
                                                                                                                                                                   The present sequence is the protein sequence for serine/threonine dehydrase 37. The dehydrase and its coding sequence are useful for treating diseases e.g. cancer and HIV infection.
                                                                                                                                                                                                                                                                                            Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VSPEVKNVCIVLSGGNVDLT-SLNWVGQAERPAPYQTVSV 339
                                                                                                                                                                                                                                                                                        DB 22;
                                                                                                                                                                                                                                                                                   90.5%; Score 1574.5; DB 27
ilarity 89.4%; Pred. No. 2.4e-152;
Conservative 19; Mismatches 16;
                                                                                                                              Claim 1; Page 27 (Disclosure); 34pp; Chinese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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          WPI; 2001-530468/59.
N-PSDB; AAI65020.
                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                 340 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAY-2002
                                                                                                                                                                                                                                                                                                                            fatches 304;
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                                                                                                                                                                                                                                                   Sequence
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RESULT 8 ABB89713

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us-09-889-609b-8.rag

Homo sapiens.

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                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISFHDVTSAAFLIRGGVERTP-CPKSTSSDLYGMELYLKKDFLQYTGSFKERGARYALLS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGASIV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPP--ETIADGVK-S:242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVALAAVLSQHFQTVS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 ISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNAIRG 66
                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                               New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - VDGNDMGEAKSLAMRMSREEGLLYVNGYDHPHIMAGQGTIGLEILEQVPEPDAVVVPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 YCDPSDESREKVTQRIMQETEGIL-VHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder.
                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 17916; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.0%; Score 453; DB 22;
ilarity 37.1%; Pred. No. 2.6e-37;
Conservative 47; Mismatches 139;
                                                                                                 Myers EW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human diagnostic protein #24289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - KGKKVVVLLCGGNIDTT 366
                                                                                               PWD,
              23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
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                                                                                               Adams M,
                                                                                                                               WPI; 2001-656860/75
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ses 118; Conserv
                                                            (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      469 AA;
                                                                                                                                                 N-PSDB; ABL07811
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                                                                                              JC,
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                                                                                               Venter
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polymetrase chain reaction (FR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II) repressed chain reaction (FR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymeteotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat diseases states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markets and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating the polypeptide and polyuculeotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations and to produce other types of data and products dependent on DNA and and to produce other types of data and products dependent on DNA and and cain acid sequences. ABGONOTO-BASSONOT represent novel human caid sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the inview of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 AYIVVPQTAPNCKKLAIQAYGASIV-YCDPSDESREKVTQRIMQETEGILVHPNQEPAVI 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKVVMPKGAPKSKVAATCDYSAEVVLHGDNFNDTIAKVSEIVEMEAR-IFIPPYDDPKVI 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 LFFKCELFQKTGSFKIRGALNAIRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIP 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     221 KLKGELTPNLHPPETIADGVK-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               191 FHSGEITTH-RTTGTLADGCDVSRPGNLTYEIVRELVDDIVLVSEDEIRNSMIALIQRNK 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 AGOGTIALEVLNOVPLVDALVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25.0%; Score 435.5; DB 22; Length 37.8%; Pred. No. 6.7e-35; Live 55; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to isolated polynucleotide (I) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LLIEPTAGVALAAVLSQH-----FQTVSPEVKNVCIV 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 20; SEQ ID No 54657; 103pp; English.
                                                                                                                                                                                                                                                            Tang YT;
                                                                                                                                                        2000US-0540217
2000US-0649167
                                                                                                                  30-MAR-2001; 2001WO-US08631
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Matches 105; Conservative
                                                                                                                                                                                                                                                            Liu C,
                                                                                                                                                                                                                                                                                                  WPI; 2001-639362/73
                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS88485
                                    WO200175067-A2
                                                                                                                                                        31-MAR-2000;
23-AUG-2000;
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                                                                            11-OCT-2001
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N-PSDB; AAX25334
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mourad GS;
                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                          AAY05705;
                          237
                                                                            291
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                                                                                                                                         RESULT 12
                                                                                                                                                        AAY05705
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                                                                             δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents a mutant Arabidopsis thaliana threonine dehydratase/deaminase (TD) protein of the invention. The protein is a feedback insensitive mutant. The TD DNA sequence is used as molecular marker (imparting resistance to toxic structural analogues of isoleucine) for selecting transformed cells and to produce transformants with increased levels of isoleucine (and thus better nutritional value) or of intermediates in biosynthesis of isoleucine (e.g. 2-oxobutyrate, for synthesis of the degradable biopolymer poly(hydroxybutyrate). Also repressing plants permit use of the isoleucine structural analogues as herbicides. The DNA sequences are alternatives for antibiotic resistance markers (which are potentially harmful to the environment). Since no because the contraction of the isoleucine) it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 TVVLFGDSYDQAQAHA--KIRAEEGLIFIPPPDHPDVIAGQGTVGMEITRQAKGPL-HA 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 MVKLPAD---QLAKGVICSSAGNHAQGVALSASKLGCTAVIVMPVTTPEIKWQAVENLGA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         124 SIV-YCDPSDESREKVTQRIMQETEGI-LVHPNQEPAVIAGQGTIALEVLNQV--PLVDA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 QYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNA 63
                                                                                                 Threonine dehydratase/deaminase; TD; feedback insensitive mutant; molecular marker; isoleucine toxic.structural analog resistance; isoleucine production; biosynthesis; degradable biopolymer; herbicide; polyhydroxybutyrate; antibiotic resistance marker; mutehn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding threonine dehydratase deaminase resistant to feedback inhibition, useful as selection marker for cell transformation and to impart herbicide resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21.3%; Score 371; DB 20; Length 502; 31.6%; Pred. No. 7.3e-29; ive 61; Mismatches 13.1; Indels 3
                                                                         Mutant threonine dehydratase/deaminase protein sequence.
                                                                                                                                                                                                                                                                                                                                                     Mourad GS, Pareddy DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 102-104; 194pp; English.
AAY32941 standard; Protein; 502 AA.
                                                                                                                                                                                                                                                                                                               (DOWC ) DOW AGROSCIENCES LLC. (PURD ) PURDUE RES FOUND.
                                                                                                                                                                                                                                                                          98WO-US14362.
98US-0074875.
                                                                                                                                                                                                                                                    99WO-US00560
                                                 (first entry)
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Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                     Larrinua IM, Merlo DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        should be safe to use
                                                                                                                                                                Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-527375/44.
N-PSDB; AAZ11199.
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                                                                                                                                                                                                   W09941395-A1
                                                                                                                                                                                                                                                    08-JAN-1999;
                                                                                                                                                                                                                                                                                         17-FEB-1998;
                                                09-NOV-1999
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                                                                                                                                                                             Synthetic.
                        AAY32941;
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224 QVGGFADGVAVKEVGEETFRISRNLMDGVVLVTRDAICASIKDMFEEKRNILEPAGALAL 283
180 LVVPVGGGGWVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETI--- 236
                                                 ----ADGVK-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 threonine dehydratase/deaminase (TD) which, unlike the wild-type enzyme (see AAY05702), is insensitive to feedback inhibition by isoleucine. It lacks the chloroplast transit peptide of the mutant TD precursor, and is encoded by a polynucleotide (see AAX25334) that is one of 9 calimed polynucleotides (see AAX25332-40), originally isolated and cloned from A. thaliana mutant line GM1b (omr1/omr1), which encode a feedback insensitive TD. These polynucleotides can be used to transform a wide variety of plants, fungi, bacteria and yeast. The polynucleotides differ from the wild-type only by 2 point mutations, which result in R499C and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New sequences encode mutant threonine dehydratase/deaminase - which is insensitive to feedback inhibition, useful as a selective marker to produce transformed cells resistant to toxic isoleucine analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Threonine dehydratase/deaminase; omr1 gene; feedback inhibition;
transgenic plant; selectable marker; isoleucine; mutant.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Feedback insensitive mature threonine dehydratase/deaminase.
                                                                                                                                                                                                                                                                                                               AAVLSQHFQTVSPEVKNVCIVLSGGNVDLTSLNWV 325
                                                                                                                                                                                                                                                                                                                                                                                         284 AGA-EAYCKYYGLKDVNVVAITSGANMNFDKLRIV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "Arg in wild-type enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "regulatory region R6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396..414
/note= "regulatory region
446..464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Arg in wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 60-62; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY05705 standard; Protein; 502 AA
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97US-0052096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
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LVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETI--- 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 IRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIV-YCDPSDESREKVTQRIMQETEGI-LVHPNQEPAVIAGQGTIALEVLNQV--PLVDA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----ADGVK-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVAL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 QVGGFADGVAVKEVGEETFRISRNLANDGVVLVTRDAICASIKDMFEEKRNILEPAGALAL 283
                                                                                                                                                                                                                                                                                                                    4 QYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Threonine dehydratase/deaminase; TD; feedback insensitive mutant; molecular marker; isoleucine toxic structural analog resistance; isoleucine production; biosynthesis; degradable biopolymer; herbicide; polyhydroxybutyrate; antiblotic resistance marker; mutein.
                                                                                                                                                                                                                                                                                                                                                   EYLTNILSTKVYDIAIESPLQLAKKLSKRL-----GVRMYLKREDLQPVFSFKLRGAYNM
R554H amino acid substitutions (numbering according to wild-type TD) in the R4 and R6 regulatory regions. These forms of TD are not only insensitive to feedback inhibition by isoleucine, but are also planes and microorganisms which synthesise only wild-type TD. Nucleotide sequences encoding mutated forms of TD can therefore be used to create cells that are lissensitive to compounds normally toxic to cells expressing only wild-type TD encymes, and thus may be used to provide a biochemical selectable marker. Transformants harboring a nucleotide sequence competising a promoter operably linked to a mutated TD sequence demonstrate increased levels of isoleucine production, and thus provide an improved nutrient source.
                                                                                                                                                                                                                                                                                     34;
                                                                                                                                                                                                                                                    Length 502;
                                                                                                                                                                                                                                                                                     61; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutant threonine dehydratase/deaminase protein seguence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGA-EAYCKYYGLKDVNVVAITSGANMNFDKLRIV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAVLSQHFQTVSPEVKNVCIVLSGGNVDLTSLNWV 325
                                                                                                                                                                                                                                                    Score 371; DB 20;
Pred. No. 7.3e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY32943 standard; Protein; 532
                                                                                                                                                                                                                                                    21.3%;
31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (DOWC ) DOW AGROSCIENCES LLC (PURD ) PURDUE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-US14362.
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                                                                                                                                                                                                                                                                                   Matches 106; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                       502 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09941395-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-JAN-1999;
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17-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116
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                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                   124
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This sequence represents a mutant Arabidopsis thaliana threonine dehydratass/deaminase (TD) protein of the invention. The protein is a feedback insensitive mutant. The TD DNA sequence is used as molecular marker (imparting resistance to toxic structural analogues of isoleucine) for selecting transformed cells and to produce transformants with increased levels of isoleucine (and thus better nutritional value) or of intermediates in biosynthesis of isoleucine (e.g. 2-oxobutyrate, for synthesis of the degradable biopolymer poly(hydroxybutyrate). Also TD-expressing plants permit use of the isoleucine structural analogues as herbicides. The DNA sequences are alternatives for antiblotic resistance markers (which are potentially harmful to the environment). Since no human analog of TD exists (humans can not synthesize isoleucine), it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRGLIPDTPEEKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89 MVKLPAD---QLAKGVICSSAGNHAQGVALSASKLGCTAVIVMPVTTPEIKWQAVENLGA 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIV-YCDPSDESREKVTQRIMQETEGI-LVHPNQEPAVIAGQGTIALEVLNQV--PLVDA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----ADGVK-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVAL 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 QYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYLTNILSTKVYDIAIESPLQLAKKLSKRL-----GVRMYLKREDLQPVFSFKLRGAYNM 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 LVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETI---
                                                                                                                                         resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Threonine dehydratase/deaminase, omr1 gene; feedback inhibition; transgenic plant; selectable marker; isoleucine; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.3%; Score 371; DB 20; Length 532; ilarity 31.6%; Pred. No. 8e-29; Conservative 61; Mismatches 134; Indels 34
                                                                                                                                                          to feedback inhibition, useful as selection marker for cell transformation and to impart herbicide resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feedback insensitive mature threonine dehydratase/deaminase
                                                                                                                                , nucleic acid encoding threonine dehydratase deaminase feedback inhibition, useful as selection marker for cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGA-EAYCKYYGLKDVNVVAITSGANMNFDKLRIV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  291 AAVLSQHFQTVSPEVKNVCIVLSGGNVDLTSLNWV 325
                     DR;
                        Pareddy
                                                                                                                                                                                                                                Claim 13; Page 111-114; 194pp; English.
                     Mourad GS,
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                     Larrinua IM, Merlo DJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           should be safe to use
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                                                                 WPI; 1999-527375/44
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les 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         532 AA
                                                                                           N-PSDB; AAZ11201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY05707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Loca
Matches
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Dβ
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LVVPVGGGGMVAGIAITIKALKPSVKVYAAEPSNADDCYQSKLKGELTPNLHPPETI---

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                                                                                                                                                                                                                                                This sequence represents an Arabidopsis thaliana mutant mature threonine dehydratase/deaminase (TP) which, unlike the wild-type enzyme (see AAV05702), is insensitive to feedback inhibition by soleucine. It lacks the chloroplast transit peptide of the mutant TD precursor, and is encoded by a polynucleotide (see AAX5336) that is one of 9 claimed polynucleotides (see AAX53332-40), criginally isolated and cloned from A. thaliana mutant line GMIlb (omr1/omr1), which encode a feedback insensitive TD. These polynucleotides can be used to transform a wide variety of plants, clung, bacteria and yeast. These polynucleotides differ from the wild-type only by 2 point mutations, which result in R499C and R554H amino acid substitutions (numbering according to wild-type only insensitive to feedback inhibition by isoleucine, but are also insensitive to structural analogues of isoleucine that are toxic to plants and microorganisms which synthesise only wild-type TD. Concepting experiences encoding mutated forms of TD can therefore be used to create cells that are insensitive to compounds normally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     64 IRGLIPDTPEEKPKAVVTHSSGNHCQALTYAAKLEGIPAYIVVPQTAPNCKKLAIQAYGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89 MVKLPAD---QLAKGVICSSAGNHAQGVALSASKLGCTAVIVMPVTTPEIKWQAVENLGA 145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 SIV-YCDPSDESREKVTQRIMQETEGI-LVHPNQEPAVIAGQGTIALEVLNQV--PLVDA 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYLTNILSTKVYDIAIESPLQLAKKLSKRL----GVRMYLKREDLQPVFSFKLRGAYNM 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 QYCISFADVEKAHINIQDSIHLTPVLTSSILNQIAGRNLFFKCELFQKTGSFKIRGALNA
                                                                                                                                                                                                                                                                                                                                                      New sequences encode mutant threonine dehydratase/deaminase - which is insensitive to feedback inhibition, useful as a selective marker to produce transformed cells resistant to toxic isoleucine analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             harboring a nucleotide sequence comprising a promoter operably linked to a mutated TD sequence demonstrate increased levels of isoleucine production, and thus provide an improved nutrient source.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  toxic to cells expressing only wild-type TD enzymes, and thus may
be used to provide a biochemical selectable marker. Transformants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 20: Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134; Indels
                        'note= "Arg in wild-type enzyme"
                                                                    /note= "regulatory region R4"
476..494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.3%; Score 371; DB 2
31.6%; Pred. No. 8e-29;
ive 61; Mismatches 1.
                                                                                                          /note= "regulatory region R6"
                                                   'note= "Arg in wild-type
                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 65-68; 120pp; English.
Location/Qualifiers
                                                                                                                                                                                         98WO-US14362
                                                                                                                                                                                                                    98US-0074875
                                                                                                                                                                                                                               97US-0052096
                                                                                                                                                                                                                                                            (PURD ) PURDUE RES FOUND.
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                                                                                                                                                                                                                                                                                                               WPI; 1999-120860/10.
           Misc-difference 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   532 AA;
                                                                                                                                                                                                                                                                                                                              N-PSDB; AAX25336.
                                       Misc-difference
                                                                                                                                     WO9902656-A1
                                                                                                                                                                                         10-JUL-1998;
                                                                                                                                                                                                                   17-FEB-1998;
                                                                                                                                                              21-JAN-1999
                                                                                                                                                                                                                                                                                       Mourad GS;
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                                                                    Region
                                                                                             Region
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Matches
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synthesis of the degradable biopolymer poly(hydroxybutyrate)). Also TD-expressing plants permit use of the isoleucine structural analogues as herbicides. The DNA sequences are alternatives for antibiotic resistance markers (which are potentially harmful to the environment). Since no human analog of TD exists (humans can not synthesize isoleucine), it
                       ----AMALSLHHGERVILD 253
                                                                                                                           dehydratase/deaminase (TD) protein of the invention. The protein is a feedback insensitive mutant. The TD DNA sequence is used as molecular marker (imparting resistance to toxic structural analogues of isoleucine) for selecting transformed cells and to produce transformants with increased levels of isoleucine (and thus better nutritional value) or of intermediates in biosynthesis of isoleucine (e.g. 2-oxobutyrate, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecular marker, isoleucine toxic structural analog resistance; isoleucine production; biosynthesis; degradable biopolymer; herbicide; polyhydroxybutyráte; antibiotic resistance marker; mutein.
                                                                                         ----ADGVK-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATQLVWGRMKLLIEPTAGVAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding threonine dehydratase deaminase resistant to feedback inhibition, useful as selection marker for cell transformation and to impart herbicide resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Threonine dehydratase/deaminase; TD; feedback insensitive mutant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a mutant Arabidopsis thaliana threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mutant threonine dehydratase/deaminase protein sequence.
203 IFVPVGGGGLIAGIAAYVKRVSPEVKIIGVEPADAN----
                                                                                                                                                                                                                                                         291 AAVLSQHFQTVSPEVKNVCIVLSGGNVDLTSLNWV 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mourad GS, Pareddy DR;
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Pred. No. 8.1e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY32942 standard; Protein; 539 AA
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31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (DOWC ) DOW AGROSCIENCES LLC. (PURD ) PURDUE RES FOUND.
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98US-0074875.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
Synthetic.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAZ11200
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17:FEB-1998;
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Matches	106; Conservative 61; Mismatches 134; Indels 34; Gaps 11;
Qy	ELFQKTG
qa	41 EYLTNILSTKVYDIAIESPLQLAKKLSKRLGVRMYLKREDLQPVESFKLRGAYNM 95
Οy	I PAY IVVPOTAPNCK
qa	96 MVKLPADQLAKGVICSSAGNHAQGVALSASKLGCTAVIVMPVTTPEIKWQAVENLGA 152
Qy	KVT
qa	153 TVVLFGDSYDQAQAHAKIRAEEEGLTFIPPFDHPDVIAGQGTVGMEITRQAKGPL-HA 209
Qy	DCYQSKLKGELT
qq	210 IFVPVGGGGLIAGIAAYVKRVSPEVKIIGVEPADANAMALSLHHGERVILD 260
ολ	K-SSIGLNTWPIIRDLVDDVFTVTEDEIKYATOLVWGF
qa	261 QVGGFADGVAVKEVGEETFRISRNLMDGVVLVTRDAICASIKDMFEEKRNILEPAGALAL 320
δy	291 AAVLSQHFQTVSPEVKNVCIVLSGGNVDLTSLNWV 325
qq	321 AGA-EAYCKYYGLKDVNVVAITSGANMNFDKLRIV 354
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                                                                             Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding a human serine racemase polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= a
/product= "serine racemase'
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             AAA59295
AAA59296
ABA15709
AAC10869
AAV74370
AAH98041
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ABL18395
AAZ11199
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AAZ11200
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AAX11205
AAX25340
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AAI83752
AAZ11208
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AAS82540
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AAT84000
ABL18394
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            GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                               The present sequence encodes a mammalian serine racemase, which has a specific activity of at least 0.003 micromole L.serine/mg/hour. The enzyme catalyses the direct racemisation of L.serine to peserine. D-serine appears to be an endogenous ligand of N·methyl-D-aspartate (NMDA) receptors. The mammalian serine racemases can be used to identify nedulators, which can be used in the treatment of acute or chronic neural death or dysfunction mediated by overactivation of N·methyl-D-aspartate (NMDA) receptors. Overactivation of the receptors is associated with Parkinson's disease, Huntington's disease, motor neurone
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                                                                                    which can be used to treat diseases associated with N-methyl-D-aspartate receptor overactivation, e.g. Alzheimer's disease
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            80;
                                                                         Mammalian serine racemase preparations, used to identify modulators
             Brady
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            Masaaki
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            ×
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           Sheth
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           Ή,
          Wolosker
                                          WPI; 2000-482915/42.
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                                                                                                                                                                                                                                                                                               AAACCTAGTGTGAAGGTATATGCTGCTGAACCCTCAAATGCAGATGACTGCTACCAGTCC
                         AAGCTGAAGGGGAAACTGATGCCCAATCTTTATCCTCCAGAAACCATAGCAGATGGTGTC
                                       AAATCCAGCATTGGCTTGAACACCTGGCCTATTATCAGGGACCTTGTGGATGATATCTTC
                                                                                         ACTGTCACAGAGGATGAAATTAAGTGTGCAACCCAGCTGGTGTGGGAGAGGATGAAACTA
                                                                                                                                           CTCATTGAACCTACAGCTGGTGTTGGAGTGGCTGTGTGTCTCAAACTTTTCAAACT
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/product= "Serine
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The invention relates to a recombinant polynucleotide encoding a numan serine racemase, vectors containing it, host cells expressing the racemase, wethods of identifying inhibitors of serine racemase and a transgenic animal lacking a functional endogenous serine racemase comprising the human serine racemase of the invention. The racemase comprising the human serine racemase of the invention. The racemase comprising the human serine racemase of the invention. The racemase comprising the human serine racemase of the protein and in structural studies of the protein and serine racemase cruckfunction relationships of the protein and structure/function relationships of the protein and structure/function relationships of the protein and serine racemase polymeptide have diagnostic, therapeutic or prophylactic uses (e.g. converged and mutant or polymorphic forms of the serine racemase, and the serine racemase (and serine racemase function. The polymocrebellar ataxia and schizophrenia), and would be useful for screening for modulators and/or inhibitors of serine racemase function. The polymocleotides encoding a serine racemase function, and as primers for nucleic acid emplification based assays for the detection of polymucleotides encoding serine racemase protein. The transgenic animal is useful for the study of the tissue and temporal specific animal is useful for the strine racemase gene in an animal. The gene for human serine racemase is
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                                                   "Human pyridoxal phosphate dependent enzyme"
                                                                                                                                                                                                                                                                                                                                     ACTGTCACAGAGGATGAAATTAAGTGTGCAACCCAGCTGGTGTGGGAGAGGATGAAACTA
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                  AAGCTGAAGGGGAAACTGATGCCCAATCTTTATCCTCCAGAAACCATAGCAGATGGTGTC
                                AAATCCAGCATTGGCTTGAACACCTGGCCTATTATCAGGGACCTTGTGGATGATATCTTC
                                                                                          ACTGTCACAGAGGATGAAATTAAGTGTGCAACCCAGCTGGTGGGGAGAGGATGAAACTA
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                                                                                                                                                                                                                                                       GTTTCCCCAGAAGTAAAGAACATTTGTATTGTGCTCAGTGGTGGAAATGTAGACTTAACC
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                                                                                                                          dependent enzyme 23406 which is a serine remease. Human 22406 gene is located on chromosome 17 between D178849 and D175796. The protein 22406 is a modulator of D-serine. D serine has been shown to modify behavioural changes associated with learning, memory and convulsions. Human 22046 and compounds that modulate the expression or activity are used to treat or diagnose neurodegenerative disorders including Alzheimer's disease, schizophrenia as well as quell anxiety and explicitly and prevent damage from stroke as well as cardiac (heart failure, rheumatic heart failure) and circulatory disorders, inver disorders (hepatic injury, jaundice), lung disorders, prostrate disorders (hepatic injury, jaundice), lung disorders, colon disorders (atresia, stenosis), skeletal muscle disorders (tumours-rhabdomyosarcoma) and dermal fibroblast disorders. Human 22406 cDNA is also useful in gene
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and for treatment, e.g.
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                                                                                                                                                                                                                                                                                                                                                                                   Score 1023; DB 22;
Pred. No. 3.1e-310;
0; Mismatches 0;
                             Novel polypeptide of the human pyridoxal useful in screening and detection assays
                                                                                                                   sequence is a cDNA encoding
                                                                                    Claim 1; Fig 1; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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Best Local Similarity 100.
Matches 1023; Conservative
                                                          epilepsy and Alzheimer's
P-PSDB; AAE08342
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to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 5'-end sequence of an oligonucleotide comprises a 1'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence, 3'-end sequence, sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs. The primers allow obtaining of the full-length CDNAs. The primers allow obtaining of the full-length CDNAs. The primers and methods. AAH03165 to AAH13632 and AAH13633 to AAH1364 to AAH13632 continued and page of the sequences; and AAH13632 to AAH13632
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                                                                                                                                                                                                                                                                            represent oligonucleotides, all of which are used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                          Sequence 2477 BP; 738 A; 535 C; 524 G; 680 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                     Score 1023; DB 22;
Pred. No. 3.8e-310;
0; Mismatches 0;
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100.0%;
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                                                                                                                                                                              TCCTCCATAACTTGGGTGAAGCAGGCTGAAAGGCCAGCTTCTTATCAGTCTGTTTCTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide encoding serine racemase enzyme and the enzyme useful for screening reagents regulating the activity of the enzyme in a neuron disease caused by over- or under-activation of glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of cDNA encoding human serine racemase (see AAM50262). The polynucleotide can be used in the production
                                                                                                                                                                                                                                                                                                                                                                                                         glutamate N-methyl-D-aspartate receptor; neurodegenerative disease; stroke, Alzhaimer s disease; Parkinson's disease; pain; myopathy; nootropic; neuroprotective; cerebroprotective; antiparkinsonian; analgesic; diagnosis; gene therapy; screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
52..1074
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03-APR-2000; 2000US-194249P
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                                                                                                                                                                                                                                                                                                                                                                          Human serine racemase cDNA.
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P-PSDB; AAM50262.
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P-PSDB; Key **AAI6502**C RESULT ò qq ò g ò g pp Op ŏ ŏ à g ö 120 180 240 171 231 291 351 360 411 TACGGAGCGTCAATTGTATACTGTGAACCTAGTGATGAGTCCAGAGAAAATGTTGCAAAA 420 480 531 540 591 900 651 999 711 720 9 serine racemase polynucleotides. Expression vectors and host cells are claimed. Serine racemase catalyses the conversion of L-serine to D-serine. Neuron damage following various nervous system diseases is often caused by activation of gultamate N-methyl-D-aspartate (NMDA) receptors in the brain. This receptor is activated by the binding of D-serine. Regulation of D-serine levels through regulation of serine racemase may therefore prevent or minimise neuron damage in neurogenic and myopathic disorders, mountained parkinson's disease, and disorders leading to peripheral and chronic pain. Serine racemase polypeptides and polynucleotides are used in claimed methods of screening for agents that modulate or used in claimed methods of screening for agents that modulate or 1 ATGTGTGCTCAGTATTGCATCTCCTTTGCTGATGTTGAAAAGCTCATATCAACATTCGA AATCTTTTCTTCAAATGTGAACTCTTCCAGAAAACAGGATCTTTTAAGATTCGTGGTGCT CTCAATGCCGTCAGAAGCTTGGTTCCTGATGCTTTAGAAAGGAAGCCGAAAGCTGTTGTT 421 AGAGTTACAGAAGAAACAGAAGGCATCATGGTACATCCCAACCAGGAGCCTGCAGTGATA AAGCTGAAGGGGAAACTGATGCCCAATCTTTATCCTCCAGAAACCATAGCAGATGGTGTC GATTCTATCCACCTCACACCAGTGCTAACAAGCTCCATTTTGAATCAACTAACAGGGCGC GCTGGACAAGGGACAATTGCCCTGGAAGTGCTGAACCAGGTTCCTTTGGTGGATGCACTG GTGGTACCTGTAGGTGGAGGAATGCTTGCTGGAATAGCAATTACAGTTAAAGGCTCTG AAACCTAGTGTGAAGGTATATGCTGCTGAACCCTCAAATGCAGATGACTGCTACCAGTCC decrease the activity of serine racemase. Also claimed is a pharmaceutical composition comprising either an expression vector that contains a serine racemase polynuclectide, or a reagent that modulates serine racemase enzyme activity. This is used to modulate serine racemase activity in a disease, particularly neuron damage or a neurodegenerative disease caused by the over or under-activation 0; Gaps Score 1021.4; DB 22; Length 1336; Pred. No. 8.5e-310; 0; Mismatches 1; Indels 0; or for the detection of Sequence 1336 BP; 386 A; 268 C; 319 G; 362 T; 1 other; recombinant serine racemase enzyme, 0; of the glutamate NMDA receptor 99.8%; ilarity 99.9%; Conservative (Similarity Best Local Sim Matches 1022; 112 292 Query Match 61 121 172 181 232 241 352 361 412 472 481 541 301 592 601 652 661 \$ g ŏ ò g qq ò g g ò à g ò ò g ò a ò q ò g ò g ò

1011 1071 840 900 960 951 891 Polypeptide-serine/threonine dehydrase 37 and polynucleotide for coding 712 AAGCTGAAGGGGAAACTGATGCCCAATCTTTATCCTCCAGAAACCATAGCAGATGGTGTC AAATCCAGCATTGGCTTGAACACCTGGCCTATTATCAGGGACCTTGTGGATGATATCTTC 781 ACTGTCACAGAGGATGAAATTAAGTGTGCAACCCAGCTGGTGTGGGAGAGGATGAAACTA CTCATTGAACCTACAGCTGGTGTTGGAGTGGCTGCTGTGCTGTCTCAACATTTTCAAACT GTTTCCCCAGAAGTAAAGAACATTTGTATTGTGCTCAGTGGTGGAAATGTAGACTTAAACC The present sequence is the coding sequence for serine/threonine dehydrase 37. The dehydrase and its coding sequence are useful for treating diseases e.g. cancer and HIV infection. Serine/threonine dehydrase 37; cancer; HIV infection; anti-HIV; 37" /product- "Serine/threonine dehydrase Sequence 2674 BP; 803 A; 581 C; 563 G; 727 T; 0 other; Claim 6; Page 25-26 (Disclosure); 34pp; Chinese. Serine/threonine dehydrase 37 coding sequence. Location/Qualifiers BP AAI65020 standard; cDNA; 2674 99CN-0125662. 99CN-0125662 (first entry) 262..1284 /*tag= WPI; 2001-530468/59 (UYFU-) UNIV FUDAN. TAA 1023 1072 TAA 1074 AAG78808 this polypeptide cytostatic; ss. Mao Y, Xie Y; Unidentified 21-DEC-1999; 21-DEC-1999; 27-NOV-2001 CN1300824-A. 27-JUN-2001 721 772 1021 841 901 AAI65020;

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Mammalian serine racemase preparations, used to identify modulators which can be used to treat diseases associated with N-methyl-D-aspartate receptor overactivation, e.g. Alzheimer's disease
                                                                                                                              Serine racemase; N-methyl-D-aspartate receptor; neural death; neural dysfunction; NMDA receptor; Parkinson's disease; Huntington's disease; motor neurone disease; Alzheimer's disease;
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                                                                                                              DNA encoding a murine serine racemase polypeptide
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The present sequence encodes a mammalian serine racemase, which has a specific activity of at least 0.003 micromole L-serine/mg/hour. The enzyme catalyses the direct racemisation of L-serine to D-serine. D-serine appears to be an endogenous ligand of N-methyl-D-aspartate (NMDA) receptors. The mammalian serine racemases can be used to identify modulators, which can be used in the treatment of acute or chronic neural death or dysfunction mediated by overactivation of N-methyl-D-aspartate (NMDA) receptors. Overactivation of the receptors is associated with Parkinson's disease, Huntington's disease, motor neurone
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DNA; 1018

standard;

AAA59294 AAA59294

AAA59294 RESULT

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The present sequence encodes a mammalian serine racemase, which has a specific activity of at least 0.003 micromole L-serine/mg/hour. The enzyme catalyses the direct racemisation of L-serine to D-serine. D-serine appears to be an endogenous ligand of N-methyl-D-asparate (NMDA) receptors. The mammalian serine racemases can be used to identify modulators, which can be used in the treatment of acute or chronic neural death or dysfunction mediated by overactivation of N-methyl-D-asparate (NMDA) receptors. Overactivation of the receptors is associated with Parkinson's disease, Huntington's disease, motor neurone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalian serine racemase preparations, used to identify modulators which can be used to treat diseases associated with N-methyl-D-aspartate receptor overactivation, e.g. Alzheimer's disease
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Serine racemase; N-methyl.D-aspartate receptor; neural death; neural dysfunction; NMDA receptor; Parkinson's disease; Huntington's disease; motor neurone disease; Alzheimer's disease;
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.4e-243;
es 122; I
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Pred. No. 8.4e-
0; Mismatches
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/product= "serine racemase"
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                                                                                                                                                Location/Qualifiers
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99US-0144839.
99US-0145953.
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Best Local Similarity 87.7%;
Matches 894; Conservative (
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P-PSDB; AAB07731.
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28-JUL-1999;
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Ferris CD;
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                                 CCTGCTTATATTGTGGTGCCCCAGACAGCTCCAGACTGTAAAAAACTTGCAATACAAGCC
                                         TACGGAGCGTCAATTGTATACTGTGAACCTAGTGATGAGTCCAGAGAAAATGTTGCAAAA
                                                                                          AGAGTTACAGAAGAAACAGAAGGCATCATGGTACATCCCAACCAGGAGCCTGCAGTGATA
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      -CCTCCCTGAACTGGGTGGGCAGGCTGAACGGCCAGCTCCTTACCAGACGGTCGTTT
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69 ATGTGTGCTCAGTATTGCATCTCCTTTGCTGATGTTGAAAAAGCTCATATCAACATTCGA
Query Match 11.3-Best Local Similarity 98.0 Matches 768; Conservative
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                                                                                                                                                                                   Human cDNA clone (5'-primer) SEQ ID NO:3435
                                                                                                                 BP.
                                                                                                                 AAH06600 standard; cDNA; 848
                                                                                                                                                             (first entry)
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                                                                                                                                                            26-JUN-2001
                                                                                                                                       AAH06600;
                                                                                                                                                                                                          Human;
                                                                                          RESULT 9
AAH06600
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Gaps

4 ;

DB 22; Length 848;

Score 729.2; DB 22; Length Pred. No. 3.6e-218; 0; Mismatches 12; Indels

71.3%; 98.0%;

Sequence 848 BP; 236 A; 187 C; 214 G; 207 T; 4 other;

128 120 188 180 248

9

ATGTGTGCTCAGTATTGCATCTCCTTTGCTGATGTTGAAAAGCTCATATCAACATTCGA

GATTCTATCCACCTCACACCAGTGCTAACAAGCTCCATTTTGAATCAACTAACAGGGCGC AATCTTTTTTTAAATGTGAACTCTTCCAGAAAACAGGATCTTTTAAGATTCGTGGTGCT CTCAATGCCGTCAGAAGCTTGGTTCCTGATGCTTTAGAAAGGAAGCCGAAAGCTGTTGTT CCTGCTTATATTGTGGTGCCCCAGACAGCTCCAGACTGTAAAAAACTTGCAATACAAGCC

368

360

301

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28-JUL-2000; 2000EP-0116126.

07-FEB-2001

308

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comptises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprises a squence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence. Sequence complementary to a joynucleotide which comprises a 1 east 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in gree therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the primers useful for synthesising polynucleotides, particularly without any specialised methods. AAH03166 to AAH13628 and AAH13633 cepresent human amino acid sequences; and AAH13629 to AAH13632 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                               Yamamoto J;
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Otsuki
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                                                                                                                                                                                                                                                                                                                                                       Nagai K,
                                                                                                                                                                                                                                                                                                               Hayashi K,
A, Naqai K
                                                                                                                                                                                                                                                                                                                                                       Wakamatsu
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Sugiyama T, Wakamatsu
29-JUL-1999; 99JP-0248036.
27-AG-1999; 99JP-0300253.
11-JAN-2000. 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
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AAGCTGAAGGGGAA
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                                                                                                                                                                                                                                                                                                                                                       Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antialergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antidererial; antifungal; antiparastiic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; gene; ss.
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   TACGGAGCGTCAATTGTATACTGTGAACCTAGTGATGACGAGAAAATGTTGCAAAA
           AAATCCAGCATTGGCTTGAACACCTGGCCTATTATCAGGGACCTTGTGGATGATATCTTC
                                                                                                                                                                                                         AGAGTTACAGAAGAAACAGAAGGCATCATGGTACATCCCAACCAGGAGCCTGCAGTGATA
                                                                    GCTGGACAAGGGACAATTGCCCTGGAAGTGCTGAACCAGGTTCCTTTGGTGGATGCACTG
                                                                            GTGGTACCTGTAGGTGGAGGAATGCTTGCTGGAATAGCAATTACAGTTAAGGCTCTG
                                                                                                                                   AAACCTAGTGTGAAGGTATATGCTGCTGAACCCTCAAATGCAGATGACTGCTACCAGTCC
                                                                                                                                                                   AAGCTGAAGGGGAAACTGATGCCCAATCTTTATCCTCCAGAAACCATAGCAGATGGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel 1405 isolated polypeptides, useful for diagnosis, treatment and prevention of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative
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                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90444) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast on ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                               Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AIGTGTCTCAGTATTGCATCTCCTTTGCTGATGTTGAAAAGCTCATATCAACATTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATCTTTTCTTCAAATGTGAACTCTTCCAGAAAACAGGATCTTTTAAGATTCGTGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTGCTTATATTGTGTGCCCCCAGACAGCTCCAGACTGTAAAAAACTTGCAATACAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACGGAGCGTCAATTGTATACTGTGAACCTAGTGATGAGTCCAGAGAAAATGTTGCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGAGTTACAGAAGAAACAGAAGGCATCATGGTACATCCCAACCAGGAGCCTGCAGTGATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTGGACAAGGGACAATTGCCCCTGGAAGTGCTGAACCAGGTTCCTTTGGTGGATGCACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                          204 A; 158 C; 184 G; 178 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.1%; Score 645.6; DB 24
99.0%; Pred. No. 5.9e-192;
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Matches 667; Conserv
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AA-GAGTTACAGAAGAAACAGAAGGCATCATGGTACATCCCAACCAGGGGGCCTGCAGTGA 478
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CCTGCTTATATTGTGGGGCCCCAGACAGCTCCAGACTGTAAAAAACTTGCAATACAAGCC
                                                                                                                                                                                TACGGAGCGTCAATTGTATACTGTGAACCTAGTGATG-AGTCCAGAGAAATGTTGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a fragment of a mammalian serine racemase gene. The racemase polypeptide has a specific activity of a least 0.03 micromole L-serine/mg/hour. The enzyme catalyses the direct racemisation of L-serine to D-serine D-serine appears to be an endogenous ligand of N-methyl-D-aspartate (NMDA) receptors. The
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                                                                                                                                                                                                                                                                                                                                                                                    TGGTGGTACCTGTAGGTGG-AGGAGGAATGCTTGCTGGAA 577
                                                                                                                                                                                                                                                                                                                                                                                                     C-terminal sequence of human serine racemase DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 18; Page 27; 54pp; English.
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99US-0144839.
99US-0145953.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA59296 standard;
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Ferris CD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which can be used to treat diseases associated with
N-methyl-D-aspartate receptor overactivation, e.g. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 ATGTGTGCTCAGTATTGCATCTCCTTTGCTGATGTTGAAAAGCTCATATCAACATTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATCTTTTCTTCAAATGTGAACTCTTCCAGAAAACAGGATCTTTTAAGATTCGTGGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     racemase gene. The racemase polypeptide has a specific activity of at least 0.003 micromole L-serine/mg/hour. The enzyme catalyses the direct racemisation of L-serine to D-serine. D-serine appears to be an endogenous ligand of N-methyl-D-aspartate (MMDA) receptors. The mammalian serine racemases can be used to identify modulators, which can be used in the treatment of acute or chronic neural death or dysfunction mediated by overactivation of N-methyl-D-aspartate (NMDA) receptors. Overactivation of the receptors is associated with Parkinson's disease, Huntington's disease, motor neurone disease and Alzheimer's disease.
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                                                                                                                                                                                            Serine racemase; N-methyl-D-aspartate receptor; neural death; neural dysfunction; NMDA receptor; Parkinson's disease; Huntington's disease; motor neurone disease; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence represents a fragment of a mammalian serine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 608 BP; 174 A; 137 C; 148 G; 148 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masaaki T,
                                                                                                                                                             N-terminal sequence of human serine racemase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sheth K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 17; Page 26; 54pp; English.
                                                                BP.
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99US-0144839.
99US-0145953.
                                                                DNA; 608
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                                                                                                                                 entry)
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                                                              AAA59295 standard;
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les 571; Conserv
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                                                                                                                                                                                                                                                                Homo sapiens
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CD;
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                                                                                                                                                                                                                                                                                                                        Human: nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiuticer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurological disease; infection; nephrotropic; gene therapy; vaccine; ds
        can be used in the treatment of acute or chronic neural death or dystunction mediated by overactivation of N-methyl-D-aspartate (NMDA) receptors. Overactivation of the receptors is associated with Parkinson's disease, Huntington's disease, motor neurone disease and Alzheimer's disease.
                                                                                                                                       676 CTGATGCCCAATCTTTATCCTCCAGAAACCATAGCAGATGGTGTCAAATCCAGCATTGGC
                                                                                                                                                                                 736 TTGAA-CACCTGGCCTATTATCAGGGACCTTGTGGATGATATCTTCACTGTCACAGAGGA
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                                                                                                                                                                                                                                                                     AGCTGGTGTTGGAGTGGCTGCTGTGTCTCAACATTTTCAAACTGTTTCCCCAGAAGT
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mammalian serine racemases can be used to identify modulators, which
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                                                                                                                                                                                                                                                                                                                                                        GGTGAAGCAGGCTGAAAGGCCCAGCTTCTTATCAGTCTGTTTCTGTTTAA 1023
                                                                                                                                                                                                                                                                                                                                                                   Score 337; DB 21; Length 509;
Pred. No. 3.7e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human nervous system related polynucleotide SEQ ID NO 8040.
                                                                                                                     0; Indels
                                                                        Sequence 509 BP; 139 A; 90 C; 115 G; 164 T; 1 other;
                                                                                                                    Mismatches
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ID ABA15709 standard; DNA; 20892 BP
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99.7%;
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Matches 348;
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The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABB14678-ABB18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 8040; 1701pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001US-0259678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for preventing, cancers and metastases
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          marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes melitius, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and parasitic infections.

Note: The sequence data for this patent did not form part of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTGTATTGTGCTCAGTGGTGGAAATGTAGACTTAACCTCCTCCATAACTTGGGTGAAGC
                                                                                                                                                      Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5' ESTs derived from
 and ovarian cancer and other cancers of the adrenal gland, bone, bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                             DB 22; Length 20892;
                                                                                                                                                                                                                           Sequence 20892 BP; 5768 A; 4125 C; 5164 G; 5835 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12614 AGGCTGAAAGGCCAGCTTCTTATCAGTCTGTTTTAA 12574
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                                                                                                                                                                                            from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                           Score 221; DB 22
Pred. No. 8e-58;
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Matches 221; Conservative
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from noligo-dry primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                      GATGAGTCCAGAGAAAATGTTGCAAAAAGAGTTACAGAAGAAAAAAGAAGGCATCATGGTA 453
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                                                                                                                                                                                                                                                                                                                                                                                  CATCCCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGGACAATTGCCCTGGAAGTGCTG
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                                                                                                                                                                                                         Sequence 861 BP; 257 A; 167 C; 240 G; 191 T; 6 other;
                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                          Score 200.2;
Pred. No. 4.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents one of 5191 Staphylococcus aureus DNA sequences of the invention. The DNA sequences are recorded on a computer readable medium, preferably selected from a floppy or hard disk, random access memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using the S.aureus DNA sequences allows putative functions to be assigned so that protein-encoding or regulatory regions of commercial, therapeutic or industrial importance can be obtained. Specifically, sequences which are likely to encode antigens have been identified and these polypeptides can be used in a vaccine composition against S.aureus infection. The polypeptides can also be used in a kit for the immunodetection of S.aureus in a sample. S.aureus is implicated in numerous human diseases, including cellulitis, eyelld infections, food poisoning, osteomyelitis, syndrome, etc. Organisms transformed with the DNA sequences can be used for recombinant production of the polypeptides. The new DNA sequences contained on the computer readable madium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1261 TCGAAGAAGCTAAAGCAAGCATTAAACCATTTATTCGTCGAACACCTCTAATTAAATCAA 1320
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                                                                                            these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence
these bases represent a line of missing text in the sequence listing in the specification. They are included to maintain the nucleotide numbering given in the specification for this DNA sequence.
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                                                                                                                                                                                                                                                                                                                                         Kunsch CA;
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0; Mismatches 468;
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Pred. No. 3.1e-32;
                                                                                                                                                                                                                                                                                                                                    Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                                                                  Polynucleotide(s) and proteins derived from stored on computer readable medium and used anti-S.aureus vaccines
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Best Local Similarity 48.5
Matches 450; Conservative
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Search completed: June 24, 2003, 09:44:54 Job time : 289 secs

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Sequence 1928,

Sequence 21, Applisequence 21, Applisequence 27, Applisequence 2742, Applisequence 21356, Applisequence 59, Applisequence 28, Applisequence 28, Applisequence 212, Applisequence 212, Applisequence 210, Applisequence 5803, Appli

0 US-09-974-300-1928 0 US-09-921-823-18 0 US-09-921-823-18 0 US-09-921-823-51 0 US-09-921-823-51 0 US-09-938-8428-271 0 US-09-938-8428-3356 0 US-09-938-8428-3356 0 US-09-938-8428-3356 0 US-09-938-8428-3356 0 US-09-938-8428-355 0 US-10-153-568-28 0 US-10-153-568-28 0 US-10-153-568-455 0 US-10-088-841-212 0 US-09-822-8498-212 0 US-09-822-8498-212 0 US-09-822-8498-212

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Sequence 10, Appl Sequence 1, Appli

US-02-764-891-5804 US-09-764-891-5803 US-09-918-995-32623 US-09-918-802-75 US-09-738-626-1101 US-10-198-846-5906 US-10-198-846-5906 US-09-738-626-1

ALIGNMENTS

US/08/781,986A

PB248PP

LENGTH: 31096 base pairs TYPE: nucleic acid STRANDEDNESS: double

linear

; TOPOLOGY: US-08-781-986A-59

Sequence 49, Requence 47, Requence 50, R

Seguence 46,

Sequence 207

US-09-974-300-4809

US-08-781-986A-102 US-09-939-980-207

US-10-234-432-47 US-10-234-432-50 US-10-234-432-46

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SEQUENCE CHARACTERISTICS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Human Genome Sciences, Inc
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 59, Application US/08781986A; Publication No. US20030054436A1
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REGISTRATION NUMBER: 30,446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 59.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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CITY: Rockville
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STATE: Maryland
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867.232 Million cell updates/sec
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                                                                                                        June 24, 2003, 06:21:15 ; Search time 1731 Seconds
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Compugen Ltd
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US-09-738-626-1091
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US-10-329-960-1
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             GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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TITLE OF INVENTION: Uncleotide Sequence of the Haemophilus influenzae Rd Genome,
TITLE OF INVENTION: Thereof, and Uses Thereof
FILE REFERENCE: PB186P1
CURRENT APPLICATION NUMBER: US/10/329,960
CURRENT FILING DATE: 2003-01-02
PRIOR PAPLICATION NUMBER: US 09/643,990
PRIOR PLING DATE: 2000-08-23
PRIOR PLING DATE: 1995-06-07
PRIOR PLING DATE: 1995-06-07
PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Haemophilus influenzae
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LOCATION: (4747)..(4747)
OTHER INFORMATION: n equals
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                                                                                                    1311 ATTAAATCAATGTATTTAAGCCAAAGTATAACTAAAGGGAATGTATTTCTAAAATTAGAA 1370
                                                                                                                                                                                                                                                      1784 GGATTAATTGCAGGTATTGCCACCGCATTAAAATCATTTAACCCTTCAATTCATATTATC 1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1544 GAAACAGCACCACAAGCGAAACAACAAGCAACAAAGGCTATGGGGCAAAGGTTATTTA 1603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2024 GAACATGCTATGAAAGATTTAATGCAGCGTGCCAAAATTATTACTGAAGGTGCAGGCGCA 2083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2084 TTACCAACAGCTGCAATTTTAAGTGGAAAAATAAACAATAAATGGCTTGAAGATAAAAT 2143
                                                                                                                                                                                                                                    201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1904 GAACATCGAGTGGATAGCACAATAGCAGATGGTTGTGATGTAAAAGTTCCTGGTGAACAA 1963
                                                                                                                                                                                                                                                                                                                  261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAGACAGCTCCAGACTGTAAAAACTTGCAATACAAGCCTACGGAGCGTCAATTGTATAC 381
                                                                                                                                                                                                                                                                                                                                                                                        GGCCAGGCTCTCACCTATGCTGCCAAATTGGAAGGAATTCCTGCTTATATTGTGGTGCCC 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            382 TGTGAACCTAGTGATGAGTCCAGAGAAATGTTGCAAAAAGAGTTACAGAAGAAACAGAA 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGAATGCTTGCTGGAATAGCAATTACAGTTAAGGCTCTGAAACCTAGTGTGAAGGTATAT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              862 GTTGGAGTGCTGCTGTGTCTCAACATTTTCAAACTGTTTCCCCCAGAAGTAAAGAAC 921
                                                                                84
                                                                            25 TTTGCTGATGTTGAAAAAGCTCATATCAACATTCGAGATTCTATCCACCTCACAGTG
                                                                                                                                                                                                                                  142 CTCTTCCAGAAAACAGGATCTTTTAAGATTCGTGGTGCTCTCAATGCCGTCAGAAGCTTG
                                                                                                                                                                                                                                                                                                            GTTCCTGATGCTTTAGAAAGGAAGCCGAAAGCTGTTGTTACTCACAGCAGTGGAAACCAT
                                                                                                                                                                                                                                                                                                                                                  1424 ATCACTTAACAGATGAACAAAAAGAAAAAGGCATTATCGCAGCATCTGCTGGGGAACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442 GGCATCATGGTACATCCCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGGACAATTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              502 CTGGAAGTGCTGAACCAGGTTCCTTTGGTGGATGCACTGGTGGTACCTGTAGGTGGAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    802 AAGTGTGCAACCCAGCTGGTGTGGGAGGATGAAACTACTCATTGAACCTACAGCTGGT
                                                                                                                                                        85 CTAACAAGCTCCATTTTGAATCAA----CTAACAGGGCGCAATCTTTTCTTCAAATGTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            682 CCCAATCTTTATCCTCCAGAAACCATAGCAGATGGTGTCAAATCCAGCATTGGCTTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          742 ACCTGGCCTATTATCAGGGACCTTGTGGATGATATCTTCACTGTCACAGAGGATGAAATT
                                          10; Gaps
Length 31096;
                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        922 ATTTGTATTGTGCTCAGTGGTGGAAATGTAGACTTAAC 959
Score 143.4; DB 7;
Pred. No. 2.4e-34;
0; Mismatches 472;
14.0%;
                                      Conservative
                      Similarity
                                    Matches 456;
                                                                                                                                                                                                                                                                                                            202
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or or ör or or or or or or σ σ σ ίι, ď á a. NAME/KEY: misc_feature LOCATION: (10150)..(10150) OTHER INFORMATION: n equals LOCATION: (9921)..(9921) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (29298)..(29298) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (36543)..(36543) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (36551)..(36551) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (36636)..(36636) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (40808)..(40810) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (44416)..(44416) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (45732)..(45732) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (44905)..(44905) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (44975)..(44975) OTHER INFORMATION: n equals LOCATION: (45593)..(45593) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (9921)..(992 NAME/KEY: misc_feature LOCATION: (45593)..(455 NAME/KEY: misc_feature

Sequence 1, Application US/10329960 Publication No. US20030099277A1

US-10-329-960-1

RESULT 2

794345 GTGTTGTTGCACGGTGCTAATTTCGATGAAGCCAAAAGCAAAAGCCATCGAGCTTTCAAAA 794404 313 GTGGTGCCCCAGACAGCTCCAGACTGTAAAAACTTGCAATACAAGCCTACGGAGCGTCA 372 373 ATTGTATACTGTGAACCTAGTGATGAGTCCAGAGAAAATGTTGCAAAAAGAGTTACAGAA 432 433 GAAACAGAAGGCATCATGGTACATCCCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGG 492 Ouery Match 8.7%; Score 89.4; DB 9; Length 1 Best Local Similarity 46.4%; Pred. No. 8.7e-16; Matches 291; Conservative 0; Mismatches 336; Indels υ U υ ပ NAME/KEY: misc_feature LOCATION: (147197)..(147197) OTHER INFORMATION: n equals a, t, g or or g or org or g or g or б ģ FEATURE:
NAME/KEY: misc_feature
LOCATION: (145942). (145942)
OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (150841)..(150841) OTHER INFORMATION: n equals a, t, OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (145171)..(145171) OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (131340)..(131340) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (139910)..(139910) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature LOCATION: (131360)..(131360) OTHER INFORMATION: n equals a, ď NAME/KEY: misc_feature LOCATION: (142750)..(142750) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (152530)..(152530) NAME/KEY: misc_feature LOCATION: (122336)..(122336) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (140398)..(140398) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (145058)..(145058) OTHER INFORMATION: n equals NAME/KEY: misc_feature LOCATION: (152500)..(152500) OTHER INFORMATION: n equals FEATURE: FEATURE FEATURE: FEATURE FEATURE: qq g δ Óγ g òγ

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Gaps

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NAME/KEY: misc_feature LOCATION: (119750)..(119750) OTHER INFORMATION: n equals a, t,

NAME/KEY: misc_feature LOCATION: (119924)..(119924) OTHER INFORMATION: n equals a, t,

NAME/KEY: misc_feature LOCATION: (120038)..(120038) OTHER INFORMATION: n equals a,

NAME/KEY: misc_feature LOCATION: (121344)..(121344) OTHER INFORMATION: n equals

NAME/KEY: misc_feature LOCATION: (122167)..(122167)

Length 1830121;

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343 AAACTTGCAATACAAGCCTACGGAGCGTCAATTGTATACTGTGAACCTAGTGATGAGGTCC 402
                                                                                                                                                                                                                                                                                                      403 AGAGAAAATGTTGCAAAAAGAGTTACAGAAGAAACAGAAGGCATCATGGTACATCCCAAC 462
                            223 AAGCCGAAAGCTGTTGTTACTCACAGCAGTGGAAACCATGGCCAGGCTCTCACCTATGCT 282
                                                                                                                                                                                                                                                                                                                                                                                              463 CAGGAGCCTGCAGTGATAGCTGGACAAGGGACAATTGCCCTGGAAGTGCTGAACCAGGTT 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1800 AATAATTTTGATGTTGTTTTGTTCCGGTGGGAGGAGGAGGTATTCTAGCTGGTGTATC 1858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 TGTTTGGTTGAAATTAGAAACATTACAGCCGAGCGGCTCATTTAAGCTCCGCGGGGGGT 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 CAATGCCGTCAGAAGCTTGGTTCCTGATGCTTTAGAAAGGAAGCCGAAAGCTGTTGTTAC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       303 TGCTTATATTGTGGTGCCCCAGACAGCTCCAGACTGTAAAAAACTTGCAATACAAGCCTA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGGAGCGTCAATTGTATACTGTGAACCTAGTGATGAGTCCAGAGAAAATGTTGCAAAAAG 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               344 CGGGGCAACAATAACCGTGACAGGGCGCAGCCAAGATGAAGCAGGCGCAGCCTGTATCCG 403
                                                                                                                                                                                                                                                         ATAAAAGATGTAAAAAGATTTGGAGCCAAAATACTCCAACATGGGGACAACGTAGATGCA
                                                                                                                      283 GCCAAATTGGAAGGAATTCCTGCTTATATTGTGGGGCCCCAGACAGCTCCAGACTGTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 TCTTTTCTTCAAATGTGAACTCTTCCAGAAACAGGATCTTTTAAGATTCGTGGTGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 GAACGTGCTC-----TTGTCTATGTCAGAAGGGCAAAAAGGCGTTGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Multiple Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 70.6; DB 10;
Pred. No. 6.8e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Berka, Randy M.
APPLICANT: Clausen, 1b Groth
TITLE OF INVENTION: Methods For Monitoring
TITLE OF INVENTION: Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Expression
THE REPERBREC: 10085.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 09/680,598
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 06/279,526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 8481
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4749, Application US/09974300 Patent No. US20020146721A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA; ORGANISM: Bacillus clausii
US-09-974-300-4749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 248; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-974-300-4749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 4749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS: Beja,O., Aravind,L., Koonin,E.V., Suzuki,M.T., Hadd,A.,Nguyen,L.P., AUTHORS: Jovanovich,S.B., Gates,C.M., Feldman,R.A., DeLong,E.F
TITLE: Bacterial rhodopsin: evidence for a new type of phototrophy in the sea
                          794585 AAAATCATCGGTGTAGAATCAAAGGATTCTGCGTGCTTAAAAGCGGCTCTCGATAAAGGC 794644
                                                                                                                                                                                                                                                                                                                                                                                                 794765 GACGAAGTATGCGCAGCAATGAAAGATTTGTTTGAGAACGTTCGTGCTGTTGCAGAACCA 794824
                                                                                                                                                                                                                                                                                                                       794645 GAACCAACAGATTTAACCCATATTGGATTATTTGCCGATGGCGTTGCTGTAAAACGCATT 794704
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                                                                                                                                                                                                                                                                            673 AAACTGATGCCCAATCTTTATCCTCCAGAAACCATAGCAGATGGTGTCAAATCCAGCATT 732
                                                                                                                                                                                                                                                                                                                                                                    733 GGCTTGAACACCTGGCCTATTATCAGGGACCTTGTGGATGATATCTTCACTGTCACAGAG 792
ACAATTGCCCTGGAAGTGCTGAACCAGGTTCCTTTGGTGGATGCACTGGTGGTACCTGTA 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DeLong, Edward
APPLICANT: Beja, Oded
TITLE OF INVENTION: Light-driven energy generation using proteorhodopsin
FILE OF INVENTION: Light-driven energy generation using proteorhodopsin
FILE REFERENCE: MAD 101
CURRENT APPLICATION NUMBER: US/09/847,513A
PRIOR APPLICATION NUMBER: 60/201,602
PRIOR APPLICATION NUMBER: 60/201,602
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 655
                                                                                          553 GGTGGAGGAGGAATGCTTGCTGGAATAGCAATTACAGTTAAGGCTCTGAAACCTAGTGTG
                                                                                                                                                                                    613 AAGGTATATGCTGCTGAACCCTCAAATGCAGATGACTGCTACCAGTCCAAGCTGAAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            793 GATGAAATTAAGTGTGCAACCCAGCTGGTGTGGGAGGATGAAACTACTCATTGAACCT
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LOCATION: (1593)..(2807)
OTHER INFORMATION: Predicted threonine dehydratase.
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51.0%; Pred. No. 9.7e-13;
tive 0; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: gene
LOCATION: (50866)..(51615)
OTHER INFORMATION: Proteorhodopsin gene sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              794825 TCAGGTGCATTAGGTTTGGCTGGTTTG 794851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DATABASE ACCESSION NUMBER: AF279106
DATABASE ENTRY DATE: 2000-06-15
RELEVANT RESIDUES: (50866)..(51615)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09847513A Publication No. US20030104375A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.6
Best Local Similarity 51.0
Matches 183; Conservative
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PAGES: 1902-1906
DATE: 2000-09-15
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467 GCGTCATTGGGCTAGAAATTGTCGAAGATCTTCCCGACGTTGACACCATCGTGGTTGCTG 526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR REPLICATION NUMBER: JP 09/377484
PRIOR PILING DATE: 1999-12-16
PRIOR REPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                         527 TCGGTGGCGGTGACTCTATGCAGGAATCGCA
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US-09-738-626-1
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US-09-942-891-1
; Sequence 1, Application US/09942891
; Publication No. US20030028917A1
                                                                                                                                                                                              Sequence 1, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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Best Local Similarity 50.6%;
Matches 168; Conservative
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OCHIAI, KEIKO
YOKOI, HARUHIKO
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SENOH, AKIHIRO
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LENGTH: 3309400
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APPLICANT:
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                                                              404 CCACTGTCAGCAAACAGGGCAGACGCTCGTCCCACCATTTGACGACGACAGGATTATCGC 463
                                                                                                                                                                                            543 GGTACCTGTAGGTGGAGGAATGCTTGCTGGAATAGCAATTACAGTTAAGGCTCTGAA 602
                  AGTTACAGAAGAAACAGAAGGCATCATGGTACATCCCAACCAGGAGCCTGCAGTGATAGC 482
                                                                                                         483 TGGACAAGGGACAATTGCCCTGGAAGTGCTGAACCAGGTTCCTTTGGTGGATGCACTGGT
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Pred. No. 1.4e-11;
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
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Publication No. US20020197605A1
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Best Local Similarity 50.6%;
Matches 168; Conservative (
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ANDO, SEIKO
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OCHIAI, KEIKO
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SOFTWARE: PatentIn ver. 3.0
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US-09-738-626-1091
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US-09-738-626-1091
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LENGTH: 930
                    423
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APPLICANT:
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APPLICANT: Milesky, Timochy Ambert
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APPLICANT: Kishore, Ganesh Mutthy
APPLICANT: Kishore, Ganesh Mutthy
APPLICANT: Stater, Steephen Charles
APPLICANT: Stark, David Martin
TITLE OF INVENTION: Methods of Optimizing Substrate Pools and Biosynthesis of Poly
TITLE OF INVENTION: Methods of Optimizing Substrate Pools and Biosynthesis of Poly
TITLE OF INVENTION: Mydroxybutyrate-co-poly-beta-hydroxyvalerate in Bacteria and
FILE REFERENCE: 11899.0155.DVUS02 (MOBT:155--3)
CURRENT APPLICATION NUMBER: US 09/313,123
PRIOR APPLICATION NUMBER: US 08/613,388
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: US 08/628,039
PRIOR PILING DATE: 1996-04-04
PRIOR FILING DATE: 1996-04-04
PRIOR FILING DATE: 1996-04-13
PRIOR FILING DATE: 1996-03-13
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Pred. No. 2.3e-07;
0; Mismatches 330;
                    Sequence 5, Application US/09942891
Publication No. US20030028917A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
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Best Local Similarity 43.6%;
Matches 255; Conservative
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                                                                            APPLICANT: Padgette, Stephen Rogers
APPLICANT: Stark, David Martin
TITLE OF INVENTION: Methods of Optimizing Substrate Pools and Biosynthesis of Poly-be
TITLE OF INVENTION: Hydroxybutyrate-co-poly-beta-hydroxyvalerate in Bacteria and Pla
FILE REFERENCE: 11899,0155,DVUS02 (MOBT:155--3)
CURRENT APPLICATION NUMBER: US/09/942,891
CURRENT FILING DATE: 2002-02-01
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PRIOR APPLICATION NUMBER: US 09/313,123
PRIOR APPLICATION NUMBER: US 09/313,123
PRIOR FILING DATE: 1996-06-18
PRIOR FILING DATE: 1996-06-28
PRIOR APPLICATION NUMBER: US 08/628,039
PRIOR FILING DATE: 1996-04-04
PRIOR FILING DATE: 1996-04-04
PRIOR FILING DATE: 1996-03-13
NUMBER OF SEQ ID NOS: 11
SEQ ID NO 1
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43.6%; Pred. No. 2
Gruys, Kenneth James
Mitsky, Timothy Albert
Kishore, Ganesh Murthy
Slater, Steven Charles
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255; Conservative
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APPLICANT: Gruys, Kenneth James
APPLICANT: Gruys, Timothy Albert
APPLICANT: Mitsky, Timothy Albert
APPLICANT: Mitsky, Timothy Albert
APPLICANT: Mitsky, Timothy Albert
APPLICANT: Slater, Saneward Murtin
APPLICANT: Stark, David Martin
APPLICANT: Stark, David Martin
TITLE OF INVENTION: Mydroxybutytate-co-poly-beta-hydroxyvalerate in Bacteria and
FILE REFERENCE: 11899, 0155. DVUS02 (MOBT:155--3)
CURRENT APPLICATION NUMBER: US/09/942.891
PRIOR APPLICATION NUMBER: US/09/313,123
PRIOR APPLICATION NUMBER: US/08/6713,388
PRIOR PILING DATE: 1996-06-28
PRIOR PILING DATE: 1996-06-28
PRIOR PILING DATE: 1996-06-30
PRIOR PILING DATE: 1996-04-30
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Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                 Sequence 8, Application US/09942891; Publication No. US20030028917A1; GENERAL INFORMATION:
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Best Local Similarity 43.6%;
Matches 255; Conservative
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SOFTWARE: PatentIn, version 3.1
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US-09-942-891-8
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                Indels
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0; Mismatches 330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 57;
Pred. No. 2
                                                                                                                                                    Sequence 7, Application US/09942891
Publication No. US20030028917A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: Synthetic US-09-942-891-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 43.69
Matches 255; Conservative
                                                                                                                                                                                         GENERAL INFORMATION:
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QY 427ACAGAAGAAACAGAAGGCATCATGGTACATCCCAACCAGGAGCCTGCAGTGATAG 481 I	TGAAACCTAGTĠTGAAGGTATATGCTGCTGAACCCTCAAATGCAGATGACTGCTACCAGT	Oy 659 CCAAGCTGAAGCGGAAACTGATGCCCAATCTTTATCCTCCAGAAACCATAGCAGTGGTG 718 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 3 3 3 3 3 3	RESULT 12 US-09-939-964-1 ; Sequence 1, Application US/0993964 ; Publication No. US20030054522A1 ; GENERAL INFORMATION: ; APPLICANT: Rosenthal, Andre ; APPLICANT: Freiberg, Christoph ; APPLICANT: Perret, Xavier Philippe ; APPLICANT: Broughton, William John ; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic ; TITLE OF INVENTION: Plasmid	; FILE REFERENCE: CARPO068 ; CURRENT APPLICATION NUMBER: US/09/939,964 ; CURRENT FILING DATE: 2001-08-27 ; PRIOR APPLICATION NUMBER: 09/214,808 ; NUMBER OF SEQ ID NOS: 1 ; SEQ ID NO 1 ; LENTH: 536165 ; TYPE: DNA ; ORGANISM: Rhizobium US-09-939-964-1	Ouery Match Best Local.Similarity 45.3%; Pred. No. 0.0054; Batches 177; Conservative 0; Mismatches 214; Indels 0; Gaps 0; Oy 235 GTTGTTACTCACAGCAGTGGAAACCATGGCTCTCACCTATGCTCCCAAATGGAA 294
OY 576 AATAGCAATTACAGTTAAGGCTCTGAAACCTAGTGTGAAGGTATATGCTGCAACCCTC 635	OY 756 CAGGGACCTTGTGGATGATATCTTCACTGTCACAGAGGATGAAAT 800 	RESULT 11 US-09-974-300-264 ; Sequence 264, Application US/09974300 ; Patent No. US20020146721A1 ; Patent No. US20020146721A1 ; Patent No. US20020146721A1 ; PAPLICANT: Berka, Randy W. ; APPLICANT: Berka, Randy W. ; TITLE OF INVENTION: Methods For Monitoring Multiple Gene ; TITLE OF INVENTION: Expression ; FILE REFERENCE: 10085.500-US ; CURRENT APPLICATION UNDHER: US/09/974,300	PRIOR APPLICATION NUMBER: 09/680, 598 PRIOR PLICATION NUMBER: 09/680, 598 PRIOR PLICATION NUMBER: 00/279, 526 PRIOR PLING DATE: 2001-03-27 NUMBER OF SEQ ID NOS: 8481 SEQ ID NO 264 LENGTH: 1251 TYPE: DNA TYPE: DNA ORGANISM: Bacillus licheniformis US-09-974-300-264	Ouery Match Best Local Similarity 44.4%; Pred. No. 5.5e-05; Matches 353; Conservative 0; Mismatches 421; Indels 21; Gaps 3; Oy 11 AGTATTGCATCTCTTTGCTGATGTTGAAAAGGCCCATATCAACATTCGAGATTCTATCC 70	OY 131 TCAAATGTGAACTCTTCCAGAAACAGGATCTTTTAAGATTCGTGGTGCTCTCAATGCG 190 127 TAAAAAGAGAAGACCTGCAGGTTGTCCGCTTTTTAAACTGAGGGCCCTATTAT 182 OY 191 TCAGAAGCTTGGTCCTGATGCTTTAGAAAGCAGAAGCGCCTATTAT 182 OY 251 GTGGAACCTTGAGTTTTAGAAAGAAACGGGGGGGTTGTTACTCACAGCA 250 183AAATTGAGCAGGTTTTCAAAAAAAAAACGGGGGGTTTCCTGCTATA 310 183AAATTGAGCAGGGTTTTCAAAAAAACGGGGGGTATTCACGGAAGA 297 OY 251 GTGGAAACCATGGCCAGGGTTTTTCCTGCAAATTGCAGGAATTACAGGAAGA 297 OY 311 TTGTGGTGCCCCAGAGGAGTCGTTTTTCCTGCAAACATCTGGGAAGA 297 OY 311 TTGTGGTGCCCCAGACGCTCCAGACTTTTTCCTGCAAACATCTGGGAAGA 357 OY 311 TAATGCCGTGGAAACATGTAAAAAATTTCCCAAGTCGAAATGTTCGGCAAGG 357 OY 371 CAATTGTAAACTGTGAACAAAAATTTCCCAAGTCGAAAAAGGGGAAGG 357 OY 371 CAATTGTAAACTGTGAACCTAGTGAAAAAATGTTCGCAAAAAAGGGCAAGCG 417

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417 ATGACGTICATCCATCCATTTAACCAAGACAAAGTGATTGCCGGGCAAGGAACAGTCGGA 476
                                                                                                                                                                                                      GGAGGAATGCTTGCTGGAATAGCAATTACAGTTAAGGCTCTGAAACCTAGTGTGAAGGTA 618
                                                                                                                                                                                                                                     TATGCTGCTGAAACCCTCAAATGCAGATGACTGCTACCAGTCCAAGCTGAAGGGGAAACTG 678
                                                                                                                                                                                                                                                                                                                                                                                                       ATGCCCAATCTTTATCCTCCAGAAACCATAGCAGATGGTGTCAAATCCAGCATTGGCTTG 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                657 GTTGAGTTAGACGAAATCGACAAATTTGTCGATGGAGCGGCTGTGAAAAAAGTCGGCGAC 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    739 AACACCTGGCCTATTATCAGGGACCTTGTGGATGATATCTTCACTGTCACAGAGGATGAA 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   799 ATTAAGIGIGCAACCCAGCIGGIGIGGAAGGAIGAAACIACICATIGAACCIACAGCI 858
     442 GGCATCATGGTACATCCCAACCAGGAGCCTGCAGTGATAGCTGGACAAGGGACAATTGCC 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 102, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences NUMBER OF SEQUENCES: 5255
CORRESPONDENCE: ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                      CTGGAAGTGCTGA - - - ACCAGGTTCCTTTGGTGGATGCACTGGTGGTACCTGTAGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Genome Sciences, Inc.
9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    859 GGTGTTGGAGTGGCTGT 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFRENCE/DOCKET NUMBER: PB24
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 102:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 15249 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Rockville
STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-781-986A-102
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                              410515 ATGGTACTGCTTCCACTGTCGGGTGGCGGCTTGCTGCAGCGTTGCAGCAGCGGTGAAG 410574
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  GTGATAGCTGGACAAGGGACAATTGCCCTGGAAGTGCTGAACCAGGTTCCTTTGGTGGAT 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 AGCTCCATTTTGAATCAACTAACAGGCGCAATCTTTTCTTCAAATGTGAACTCTTCCAG 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 GTTGTCAGATCTTTTAAAATTCGCGGCGC-----CTATTACCAAATTTCTTCGCTAT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 CAAAAGAAGAACTTGCCGCTGGC-GTTGTATGCGCAAGCGCTGGAAACCATGCACAAGGG 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 GTTGCCTATTCATGCCGCGCTTTAAAAGTCAAAGGTGTTATTTTCATGCCGACTACCACG 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         297 CCAAAGCAAAAAGTCGCACAAGTGAAATTTTTGGCAGGGACTATGTAGACGTCAGGTTA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 AGTGATGAGTCCAGAGAAAATGTT-----GCAAAAAGAGTTACAGAAGAAAAAA 441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGACTGTAAAAAACTTGCAATACAAGCCTACGGAGCGTCAATTGTATACTGTGAACCT
                                                                                               535 GCACTGGTGGTACCTGTAGGTGGAGGAATGCTTGCTGGAATAGCAATTACAGTTAAG
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                                                                                                                                                                                                                                                                                                                                                           Sequence 4809, Application US/09974300
Fatent No. US20020146721A1
GENERAL INCOMMATION:
APPLICANT: Berka, Randy M.
APPLICANT: Clausen, Ib Groth
TITLE OF INVENTION: Methods For Monitoring Multiple Gene
TITLE OF INVENTION: Expression
FILE REFERENCE: 10088.500-US
CURRENT APPLICATION NUMBER: US/09/974,300
CURRENT FILING DATE: 2001-10-05
PRIOR FILING DATE: 2000-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 4.7%; Score 48.4; DB 10;
Best Local Similarity 44.5%; Pred. No. 9.5e-05;
Matches 383; Conservative 0; Mismatches 456;
                                                                                                                                                                                                                          595 GCTCTGAAACCTAGTGTGAAGGTATATGCTG 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (1)...(926)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-4809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                            -09-974-300-4809
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LENGTH: 926
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Prokaryotic Polynucleotides,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 151 AAAACAGGATCTTTTAAGATTCGTGGTGCTCTCAATGCCGTCAGAAGCTTGGTTCCTGAT 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTTTAGAAAGGAAGCCGAAAGCTGTTGTTACTCACAGCAGTGGAAACCATGGCCAGGCT 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271 CTCACCTATGCTGCCAAATTGGAAGGAATTCCTGCTTATATTGTGGTGCCCCAGACAGCT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             344 GTTGCCTATACAGCTAAAAAACTTAAINTAAACGCTGTTATCTTTATGCCAGTCACTACA 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 CCTTNACAAAAGGTAAATCAAGTAAAGTTCTTTGGAAATAGTAACGTTGAAGTTGTACTC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31 GATGTTGAAAAAGCTCATATCAACATTCGAGATTCTATCCACCTCACACCAGTGCTAACA 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches 248; Indels
                                                                                                                       INVENTION: No. US20020082234Alel Proka: Polypeptides and Their Uses
                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                   Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
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Pred. No. 0.0011;
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/939,980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear

MOLECULE TYPE: Genomic DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 207:
US-09-939-980-207
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FILING DATE: CURNOWN>ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 27-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                           Nicholas, Richard
                                           Pratt, Julie
Reichard, Richard
                                                                                 Rosenberg, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 2698 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FELEPHONE: 610-270-4478
                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline
STREET: 709 Swedeland
       Lonetto, Michael
                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                     CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FELEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 46.5%;
Matches 231; Conservative
                                                                                                     Ward, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <Unknown>
                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 19406-0939
                                                                                                                       Q.
                                                                                                                       TITLE
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                                                       Score 46.2; DB 7;
Pred. No. 0.0031;
; Mismatches 408;
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                                               Query Match
Best Local Simil
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Novel human diagno
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99US-0144839.
.99US-0145953.
 18-JAN-2000; 2000WO-US00938
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N-PSDB; AAA59299.
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28-JUL-1999;
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Ferris CD;
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                                                                         June 24, 2003, 05:35:44 ; Search time 46.0677 Seconds (without alignments) 983.448 Million cell updates/sec
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Compugen Ltd
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          GenCore version
Copyright (c) 1993 - 2003
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Listing first 45 summaries
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                                                                                                                                                                D-serine appears to be an endogenous ligand of N-methyl-D-aspartate (NMDA) receptors. The mammalian serine racemases can be used to identify modulators, which can be used in the treatment of acute or chronic neural death or dysfunction mediated by overactivation of N-methyl-D-aspartate (NMDA) receptors. Overactivation of the receptors is associated with Parkinson's disease, Huntington's disease, motor neurone
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              Mammalian serine racemase preparations, used to identify modulators which can be used to treat diseases associated with N-methyl-D-aspartate receptor overactivation, e.g. Alzheimer's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; serine racemase; Parkinson's disease; Huntingdon's disease; anxiety; glaucoma; stroke; hyperalgesia; pain; spinocerebellar ataxia; schizophrenia; transgenic animal; chromosome 17pl3; immunogen.
                                                                                                                       racemase, which has
                                                                                                                                                                                                                                                                                                                                                                                              YGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDAL
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100.0%;
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Best Local Similarity 100.0
Matches 340; Conservative
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                                                                                                                                                                                                                                                                                        340 AA;
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human serine racemase, vectors containing it, host cells expressing the cacemase, methods of identifying inhibitors of serine racemase and a transgenic animal lacking a functional endogenous serine racemase and transgenic animal lacking a functional endogenous serine racemase comprising the human serine racemase of the invention. The racemase comprising the human serine racemase of the invention. The racemase comprising the human serine racemase of comprising the racemase comprising the human serine standing of the protein and structural studies of the protein and structural studies of the protein and construction relationships of the protein. Biologically active construction relationships of the protein. Biologically active structure/function relationships of the protein. Biologically active comprehensive and and transgenical diseases such as Parkinson's and Huntingdon's disease, anxiety, glaucoma, strucke, hyperalgesia, pain, spinocerebellar ataxia and consideration of serine racemase function. The polynucleotides are useful continuity of serine racemase function and as primers for nucleic actide amplification based assays for the detection of polynucleotides encoding conding a serine racemase protein. The transgenic animal is useful for the strine racemase protein. The transgenic animal is useful for the strine racemase protein. The present sequence represents human serine racemase gene in an animal. The gene for human serine racemase in an animal. The gene for human serine racemase conding a care of the present sequence represents human serine racemase conding and activity of the serine racemase gene in an animal. The gene conding activity of the serine racemase gene in an animal. The gene conding a serine racemase serine racemase gene in an animal The gene for human serine racemase serine racemase decomase in an animal racemase decomase is a problem of protein racemase serine racemase serine racemase serine racemase in an animal racemase serine racemase serine racemase in an animal racemase serine racemase
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                   (MERI ) MERCK & CO INC
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                                                                   anticonvulsant; cerbroprotective; cardiant; vasotropic; gene therapy; epilepsy; Alzheimer's disease; chromosome 17; serine racemase; stroke; behavioural change; neurodegenerative disorder; schizophrenia; arresia; rheumatic heart failure; circulatory disorder; hepatic injury; jaundice; lung disorder; nodular hyperplasia; stenosis; skeletal muscle disorder; tumour; rhabdomyosarcoma; dermal fibroblast disorder.
                                                           pyridoxal phosphate dependent enzyme; nootropic; neuroprotective;
                                                                                                                                                                                   "Pyridoxal-phosphate dependent enzyme family
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|abel= Casein_kinase_II_phosphorylation_site
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                                          Human pyridoxal phosphate dependent enzyme 22406 protein
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                                                                                                                                                                                                                                                                                                                             Alzheimer's disease, schizophrenia as well as quell anxiety and epilepsy and prevent damage from stroke as well as cardiac (heart failure, rheumatic heart failure) and circulatory disorders, liver disorders (hepatic injury, jaundice), lung disorders, prostrate disorders (benign enlargement, nodular hyperplasia), colon disorders (atresia, stenosis), skeletal muscle disorders (tumours-rhabdomyosarcoma) and dermal fibroblast disorders. Human 22406 cDNA is also useful in gene
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                                                                                                                                                                                                                                              is a modulator of D-serine. D serine has been shown to modify behavioural changes associated with learning, memory and convulsions. Human 22046 and compounds that modulate the expression or activity are used to treat or diagnose neurodegenerative disorders including
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGV
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                                       dependent family
                                              phosphate dependent fami and for treatment, e.g.
                                                                                                                                                                             The present sequence is human pyridoxal phosphate dependent enzyr 22406 which is a serine racemase. Human 22406 gene is located on chromosome 17 between D17849 and D178796. The protein 22406
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Mismatches 0;
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VSPEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV 340

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The present invention describes primer sets for synthesising 5602 (ill-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence of an oligonucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises at 3'-end sequence. Where the oligonucleotide which comprises as 1'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the action and/or diagnosis of the abnormality of the full-length cDNAs are primers allow obtaining of the full-length cDNAs asily without any specialised methods. AAH13628 and AAH13633 to AAH13632 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632 represent human amino acid sequences; and AAH13632 to AAH13632 represent human amino acid sequences; and the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CDNAs.
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                                                                                                                                                                                                                                                                                                                              Yamamoto J;
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Otsuki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; SEQ ID 15149; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                           Nishikawa T, Hayashi K, S
T, Wakamatsu A, Nagai K,
                                                        29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0241899.
28-JUL-2000; 2000EP-0116126
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                                                                                                                                                                                                                                                           (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                           ogai T, Nis
Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-318749/34.
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The present sequence is that of human serine racemase, an enzyme that catalyses the conversion of L-serine to D-serine. Neuron damage following various nervous system diseases is often caused by a ctivation of glutamate N-methyl-D-aspartate (NMDA) receptors in the brain. This receptor is activated by the binding of D-serine. Regulation of D-serine levels through regulation of Serine. Regulation of D-serine levels through regulation of Serine and therefore prevent or minimise neuron damage in neurogenic and may therefore prevent or minimise neuron damage in neurogenic and disease and Parkinson's disease, and disorders leading to peripheral and chronic pain. The invention provides serine racemase polypeptides and methods for their recombinant production. These polypeptides are used in claimed methods of screening for agents that modulate or decrease serine racemase activity. A claimed pharmaceutical composition comprising either an expression vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polynucleotide encoding serine racemase enzyme and the enzyme useful for screening reagents regulating the activity of the enzyme in a neuron disease caused by over- or under-activation of glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that contains a serine racemase polynucleotide, or a reagent that modulates serine racemase enzyme activity, is used to modulate serine racemase activity in a disease, particularly neuron damage or a neurodegenerative disease caused by the over- or under-activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "cysteine synthase/cystathione beta-synthase
                                                                                                                                                                                                    glutamate N-methyl-D-aspartate receptor; neurodegenerative diseass
stroke; Alzheimer's disease; Parkinson's disease; pain; myopathy;
nootropic; neuroprotective; cerebroprotective; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                    41.59
/note= "prosite serine/threonine dehydratase
                                                                                                                                                                                                                                                                                                                                                                                           pyridoxal-phosphate attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                                              pyridoxal-phosphate attachment site"
                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "serine/threonine dehydratase
                                                                                                                                                                                    Serine racemase; human; D-serine; regulation;
                                                                                                                                                                                                                                                            analgesic; diagnosis; therapy; screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      attachment site"
                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                      AA
                                    AAM50262 standard; Protein; 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 2; 66pp; English.
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2000US-194249P
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                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-methyl-D-aspartate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-64844/74.
N-PSDB; AAI70575.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ramakrishnan S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200173077-A2.
                                                                                                                                                                                                                                                                                                                                     Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                  Human serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAR-2000;
03-APR-2000;
                                                                                                           21-JAN-2002
                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-2001.
                                                                     AAM50262;
RESULT 5
AAM50262
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Gaps

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LNAVRSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQA 120
                                                                                                    YGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalian serine racemase preparations, used to identify modulators which can be used to treat diseases associated with N-methyl-D-aspartate receptor overactivation, e.g. Alzheimer's disease
                                                                                                                                                                        1 MCAQYCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGA
                                                               KSSIGLNTWP1IRDLVDD1FTVTEDEIKCATQLVWERMKLL1EPTAGVGVAAVLSQHFQT
                                                                                                                                                                                                                          neural dysfunction; NMDA receptor; Parkinson's disease;
Huntington's disease; motor neurone disease; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brady
                               ö
          Length 340;
                                                                                                                                                                                                                                                                                                                                                                                                              Serine racemase; N-methyl-D-aspartate receptor; neural death;
                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a murine serine racemase polypeptide
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                               Indels
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                                                                                                                                                                                                                                                                   VSPEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV
           DB 22;
  Score 1727; DB 22
No. 1e-166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SH, Wolosker H, Sheth K, Masaaki T,
CD;
                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                              AAB07731 standard; Protein; 339
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99US-0144839.
99US-0145953.
          99.5%;
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                                                                                                                                                                                                                                                                                                                                                                      entry)
                               Conservative
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                     Best Local Similarity
Matches 339; Conserv
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Misc-difference
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21-JUL-1999;
28-JUL-1999;
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           Query Match
Best Local 3
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                                                                                                                                  YGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGOGTIALEVLNQVPLVDAL 180
                                                                                                                                                                                  180
                                                                                 9
                                                                                                   09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide-serine/threonine dehydrase 37 and polynucleotide for coding this polypeptide -
                                                                                           VVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGV
                                                                                                                                                                                                                KSSIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQT
                                                                               1 MCAQYCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGA
                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the protein sequence for serine/threonine dehydrase 37. The dehydrase and its coding sequence are useful for treating diseases e.g. cancer and HIV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                           dehydrase 37; cancer; HIV infection; anti-HIV;
                                                           'n
                                       Length 340;
                                                             Indels
                                                                                                                                                                                                                                                                                                VSPEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV 340
                                        Score 1731; DB 22;
Pred. No. 4.1e-167;
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                                                             1; Mismatches
                                                                                                                                                                                                                                                                                                                                                             Ä
                                                                                                                                                                                                                                                                                                                                                           Protein; 340
  receptor
                                                                                                                                                                                                                                                                                                                                                                                                                       Serine/threonine dehydrase 37.
                                       99.8%;
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                                                Local Similarity 99.7
hes 339; Conservative
of the glutamate NMDA
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                                                                                                                                                                                                                                                                                                                                                           standard;
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                     340 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
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                     Sequence
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                                                                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                     LNAVRSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQA 120
                                                                                                                                                                                                                                                                               YGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDAL 180
                                                                                                                                                                                                                                                                                                                                                                                                        241 KSSIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein.
                                                                  (NMDA) receptors. The mammalian serine racemases can be used to identify modulators, which can be used in the treatment of acute or chronic neural death or dysfunction mediated by overactivation of N-methyl-D-aspartate (NMDA) receptors. Overactivation of the receptors is associated with Parkinson's disease, Huntington's disease, motor neurone
                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                 The present sequence represents a manmalian serine racemase, which has a specific activity of at least 0.003 micromole L-serine/mg/hour. The enzyme catalyses the direct racemisation of L-serine to D-serine.
                                                                                                                                                                                                                    1 MCAQYCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGA
                                                                                                                                                                                                                                                                                                                                                             VVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGV
                                                      D-serine appears to be an endogenous ligand of N-methyl-D-aspartate
                                                                                                                                                                          Length 339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSPEVKNICIVLSGGNVDLTSSITWVKQAERPASYQSVSV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 21;
                                                                                                                                                                       91.2%; Score 1582.5; DB 2189.7%; Pred. No. 5.1e-152; ive 19; Mismatches 15;
Claim 7; Page 48-49; 54pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human polypeptide SEQ ID NO 2089.
                                                                                                                             disease and Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB89713 standard; Protein; 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAY-2000; 2000US-205515P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-MAY-2001; 2001WO-US16450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                     Similarity
                                                                                                                                                    339 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 - MAY - 2002
                                                                                                                                                                                      Local Simmes 305;
                                                                                                                                                                                                                                                                                                                                    121
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                                                                                                                                                    Sequence
                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                      301
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                                                                                                                                                                                              Matches
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The invention relates to novel genes (ABL89449-ABL90853) and proteins (ABB89040-ABB90404) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colliss; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LNAVRSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 LNAVRSLVPDALERKPRAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDAL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 YGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDAL 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MCAQYCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MCAQYCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                 gastrointestinal, pulmonary, cardiovascular, renal and proliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 23; Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMP 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; SEQ ID NO 2089; 2081pp + Sequence Listing; English.
                                                                                     Novel 1405 isolated polypeptides, useful for diagnosis, tree prevention of neural, immune system, muscular, reproductive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2e-99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61.2%;
93.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and parasitic infections.
                                                                                  Novel 1405 isolated
2002-122018/16
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                            N-PSDB; ABL90122
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2000US-0540217 2000US-0649167

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30-MAR-2001; 2001WO-US08631
                                                                                                                             (HYSE-) HYSEQ INC
                      WO200175067-A2.
Homo sapiens.
                                                                                          31-MAR-2000;
23-AUG-2000;
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                                            11-OCT-2001
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                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 ISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRS 66
                                                                                                                                                                                                                                                                                             The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                            New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
                                                                                                                                                                                                                        useful in developmental biology and in elucidating cell signalling and cell.cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30311), expressed DNA sequences (ABL16176-ABL30311), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                  127 YCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           175 VDGNDMGEAKSLAMRWSREEGLLYVNGYDHPHIMAGQGTIGLEILEQVPEPDAVVVPVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SSIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQT
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                                                            Disclosure; SEQ ID NO 17916; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                    Length 469;
                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                          52; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                    25.9%; Score 450; DB 22; 36.6%; Pred. No. 1.2e-36;
                                                                   Myers EW;
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L--KGKKVVVLLCGGNIDTT 366
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                                                                   PWD,
         2000US-191637P
2000US-0614150
                                                                                                                                                                                                                                                                                                                                                                                            Matches 117; Conservative
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                                                                   Venter JC, Adams M,
                                                                                           2001-656860/75
                                                                                                                                                                                                                                                                                    ABB57737-ABB72072)
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                             (PEKE ) PE CORP NY
                                                                                                                                                                                                                                                                                                                                             469 AA;
                                                                                                      N-PSDB; ABL07811
         23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                               Sequence
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polypeptide (II) sequences. (II) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (III). The polymucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. He polypeptide and polymucleotide sequences have applications in the polyperide and polymucleotide sequences have applicated activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKLKGKLMPNLYPPETIADGVK-SSIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERM 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IAGQGTIALEVLNQVPLVDALVVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQ 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 LFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIP 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human
                                                                                                                                                                                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to isolated polynucleotide (I) and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             249 KVVTEGAGALACAALLSEAARGYEIFEKREEECRKVILV 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.9%; Score 414.5; DB 22; 36.6%; Pred. No. 2e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 20; SEQ ID No 54657; 103pp; English.
Tang YT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                         WPI; 2001-639362/73.
N-PSDB; AAS88485.
     Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1181 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 102; Conserv
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:|:| : || | | : : ::| : ::| : :| : : | 305
-ADGVK-SSIGLNTWPIIR
                                        196 EVKIIGVEPADAN-----AMALSLHHGERVILDQVGGFADGVAVKEVGEETFRISR
                                                                                    DLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVKNICIVLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents an Arabidopsis thaliana mutant mature threonine dehydratass/deaminase (TD) which, unlike the wild-type enzyme (see AAY05702), is insensitive to feedback inhibition by isoleucine. It lacks the chloroplast transit peptide of the mutant TD precursor, and is encoded by a polynucleotides (see AAX25334) that is one of 9 claimed polynucleotides (see AAX25332 (comrl/omrl), which encode a feedback insensitive TD. These polynucleotides can be used to transform a wide variety of plants, fungi, bacteria and yeast. The polynucleotides differ from the wild-type only by 2 point mutations, which result in R499C and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New sequences encode mutant threonine dehydratase/deaminase - which is insensitive to feedback inhibition, useful as a selective marker to produce transformed cells resistant to toxic isoleucine analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Threonine dehydratase/deaminase; omr1 gene; feedback inhibition; transgenic plant; selectable marker; isoleucine; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feedback insensitive mature threonine dehydratase/deaminase.
                                                                                                                                                                          -TSSITWVKQAERPASYQ 336
                                                                                                                                                                                                   1 |:: |:| |:: 306 GANMNFDKLRIVTELANVGRQQEAVLATLMPEKPGSFK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "Arg in wild-type enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Arg in wild-type enzyme"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "regulatory region R4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "regulatory region R6"
SVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 60-62; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                              AAY05705 standard; Protein; 502 AA.
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/note= "r
446..464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana.
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Misc-difference 409
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                                                                                                                                                                        314 GGNVDL---
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                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUL-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
203
                                                                                                                                                                                                                                                                                                                                                                      AAY05705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TEGI-MVHPNQEPAVIAGOGTIALEVLNQV--PLVDALVVPVGGGGMLAGIAITVKALKP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
                                                                                                                                                                                                              Threonine dehydratase/deaminase; TD; feedback insensitive mutant; molecular marker; isoleucine toxic structural analog resistance; isoleucine production; biosynthesis; degradable biopolymer; herbicide; polyhydroxybutyrate; antibiotic resistance marker; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIS STATEMENT STATEMENT STATEMENT STATEMENT SPLOLAKKLSKRLGVRMYLKREDLQPVFSFKLRGAYNMMVKLPADQL---AKGVICSSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPSDESRENVAKRVTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26 TPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding threonine dehydratase deaminase resistant to feedback inhibition, useful as selection marker for cell transformation and to impart herbicide resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21.2%; Score 368; DB 20; Length 502; 30.2%; Pred. No. 2.8e-28; ive 65; Mismatches 129; Indels 42
                                                                                                                                                                     Mutant threonine dehydratase/deaminase protein sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pareddy DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Page 102-104; 194pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mourad GS,
                                      AAY32941 standard; Protein; 502 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DOWC ) DOW AGROSCIENCES LLC. (PURD ) PURDUE RES FOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-US14362.
98US-0074875.
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                                                                                                                          09-NOV-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  should be safe to use
                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ11199
                                                                                                                                                                                                                                                                                                                                                                                         WO9941395-A1.
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Best Local Simil
Matches 102; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JAN-1999;
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17-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                             AAY32941;
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Matches
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ò QC δ g ò g Pareddy DR

Mourad GS,

Merlo DJ,

Larrinua IM,

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                                                                                                                                                                                                                                                                                                                                                                                                            DLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVKNICIVLS 313
                                                                                                                                                                                                                                                                                                                             82
                                                                                                                                                                                                                                                                                                                                                       21 SPLOLAKKLSKRLGVRMYLKREDLOPVFSFKLRGAYNMMVKLPADQL---AKGVICSSAG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         molecular marker; isoleucine toxic structural analog resistance; isoleucine production; biosynthesis; degradable biopolymer; herbicide; polyhydroxybutyrate; antibiotic resistance marker; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETI-----ADGVK-SSIGLNTWPIIR
                                                                                                                                                                                                                                                                                                                       26 TPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 TEGI-MVHPNQEPAVIAGQGTIALEVLNQV--PLVDALVVPVGGGGMLAGIAITVKALKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EVKIIGVEPADAN-----AMALSLHHGERVILDQVGGFADGVAVKEVGEETFRISR
                                                                                                                                                                                                                                                                                           Gaps
          TD) in the R4 and R6 regulatory regions. These forms of TD are not only insensitive to feedback inhibition by isoleucine, but are also insensitive to feedback inhibition by isoleucine, but are also insensitive to structural analogues of isoleucine that are toxic to plants and microorganisms which synthesise only wild type TD.

Nucleotide sequences encoding mutated forms of TD can therefore be used to create cells that are insensitive to compounds normally toxic to cells expressing only wild-type TD enzymes, and thus may be used to provide a biochemical selectable marker. Transformants harboring a nucleotide sequence comprising a promoter operably linked to a mutated TD sequence demonstrate increased levels of isoleucine production, and thus provide an improved nutrient source.
R554H amino acid substitutions (numbering according to wild-type
                                                                                                                                                                                                                                                                                           42;
                                                                                                                                                                                                                                                         Length 502;
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GANMNFDKLRIVTELANVGRQQEAVLATLMPEKPGSFK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----TSSITWVKQAERPASYQ 336
                                                                                                                                                                                                                                                        Score 368; DB 20;
Pred. No. 2.8e-28;
                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                       65;
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Best Local Similarity 30.29
Matches 102; Conservative
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                                                                                                                                                                                                                      502 AA;
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17-FEB-1998;
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dehydratase/deaminase (TD) protein of the invention. The protein is a feedback insensitive mutant. The TD DNA sequence is used as molecular marker (imparting resistance to toxic structural analogues of isoleucine) for selecting transformed cells and to produce transformants with increased levels of isoleucine (and thus better nutritional value) or of intermediates in biosynthesis of isoleucine (e.g. 2-oxobutyrate, for synthesis of the degradable blopolymer poly(hydroxybutyrate). Also FD-expressing plants permit use of the isoleucine structural analogues as herbicides. The DNA sequences are alternatives for antibiotic resistance markers (which are potentially harmful to the environment). Since no harm a malog of FD exists (humans can not synthesize isoleucine), it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TEGI-MVHPNQEPAVIAGQGTIALEVLNQV--PLVDALVVPVGGGGMLAGIAITVKALKP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETI-----ADGVK-SSIGLNTWPIIR 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVKIIGVEPADAN-----AMALSLHHGERVILDQVGGFADGVAVKEVGEETFRISR 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVKNICIVLS 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLMDGVVLVTRDAICASIKDMFEEKRNILEPAGALALAGA-EAYCKYYGLKDVNVVAITS 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPSDESRENVAKRVTEE
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                                                                                                     New nucleic acid encoding threonine dehydratase deaminase resistant to feedback inhibition, useful as selection marker for cell transformation and to impart herbicide resistance
                                                                                                                                                                                                            sequence represents a mutant Arabidopsis thaliana threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Threonine dehydratase/deaminase; omr1 gene; feedback inhibition; transgenic plant; selectable marker; isoleucine; mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Feedback insensitive mature threonine dehydratase/deaminase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.2%; Score 368; DB 20; 30.2%; Pred. No. 3.1e-28; ive 65; Mismatches 129;
                                                                                                                                                                           English
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                                                                                                                                                                      Claim 13; Page 111-114; 194pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           safe to use.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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                                                                  N-PSDB; AAZ11201
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dehydratase/deaminase (TD) protein of the invention. The protein is a feedback insensitive mutant. The TD DNA sequence is used as molecular marker (imparting resistance to toxic structural analoques of isoleucine) for selecting transformed cells and to produce transformants with increased levels of isoleucine (and thus better nutritional value) or of intermediates in biosynthesis of isoleucine (e.g. 2-oxobutyrate). Also synthesis of the degradable biopolymer poly(hydroxybutyrate)). Also TD-expressing plants permit use of the isoleucine structural analogues as markers (which are potentially harmful to the environment). Since no human analog of TD exists (humans can not synthesize isoleucine), it
                                                                                                                                              Threonine dehydratase/deaminase; TD; feedback insensitive mutant; molecular marker; isoleucine toxic structural analog resistance; isoleucine production; biosynthesis; degradable biopolymer; herbicide; polyhydroxybutyrate; antibiotic resistance marker; mutein.
                          ADGVK-SSIGLNTWPIIR
                                                                                                                  DLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVKNICIVLS
                                                                     226 EVKIIGVEPADAN------AMALSLHHGERVILDQVGGFADGVAVKEVGEETFRISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid encoding threonine dehydratase deaminase resistant to feedback inhibition, useful as selection marker for cell transformation and to impart herbicide resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence represents a mutant Arabidopsis thaliana threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutant threonine dehydratase/deaminase protein sequence.
                                                                                                                                                                                                            -TSSITWVKQAERPASYQ 336
                                                                                                                                                                                                                                                       336 GANMNFDKLRIVTELANVGRQOEAVLATLMPEKPGSFK 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pareddy DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 368; DB 20;
Pred. No. 3.1e-28;
                          SVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETI-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English
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                                                                                                                                                                                                                                                                                                                                                                            AA.
                                                                                                                                                                                                                                                                                                                                                                    AAY32942 standard; Protein; 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Page 106-109; 194pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.2%;
30.2%;
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98US-0074875
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Best Local Similarity
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                                                                                                                                                                                                          314 GGNVDL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ11200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Larrinua IM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9941395-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                       203
                                                                                                                                                                                                                                                                                                                                                                                                                  AAY32942;
                                                                                                               254
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                                                                                                                                                                                                                                                                                                                          RESULT 15
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ID AAY3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This sequence represents an Arabidopsis thaliana mutant mature threonine dehydratase/deaminase (TD) which, unlike the wild-type enzyme (see AAXO5702), is insensitive to feedback inhibition by isoleucine. It lacks the chlorophast transit peptide of the mutant TD precursor, and is encoded by a polynucleotide (see CAAX25335) that is one of 9 claimed polynucleotides (see AAX25332-40), originally isolated and cloned from A. thaliana mutant line GMILD (omr1/omr1), which encode a feedback insensitive TD. These to polynucleotides can be used to transform a wide variety of plants, fungl, bacteria and yeast. These polynucleotides differ from the wild-type only by 2 point mutations, which result in R499C and C R554H amino acid substitutions (numbering according to wild-type TD) in the R4 and R6 regulatory regions. These forms of TD are not only insensitive to feedback inhibition by isoleucine, but are also insensitive to eceback inhibition by isoleucine, but are also insensitive to a structural analogues of isoleucine that are toxic to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86 NHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPSDESRENVAKRVTEE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 TEGI-MVHPNQEPAVIAGQGTIALEVLNQV--PLVDALVVPVGGGGMLAGIAITVKALKP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26 TPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  v sequences encode mutant threonine dehydratase/deaminase - which
insensitive to feedback inhibition, useful as a selective marker
produce transformed cells resistant to toxic isoleucine analogues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plants and microorganisms which synthesise only wild-type TD.

Nucleotide sequences encoding mitated forms of TD can therefore be used to create cells that are insensitive to compounds normally toxic to cells expressing only wild-type TD enzymes, and thus may be used to provide a biochemical selectable marker. Transformants harboring a nucleotide sequence comprising a promoter operably linked to a mutated TD sequence demonstrate increased levels of isoleucine production, and thus provide an improved nutrient source.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21.2%; Score 368; DB 20; 30.2%; Pred. No. 3.1e-28; ive 65; Mismatches 129;
                                        'note= "Arg in wild-type enzyme"
                                                                                     /note= "Arg in wild-type enzyme"
                                                                                                                                                                                /note= "regulatory region R6"
                                                                                                             427..444
/note= "regulatory region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 65-68; 120pp; English.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  98US-0074875.
97US-0052096.
                                                                                                                                                                                                                                                                                                                       98WO-US14362
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Best Local Similarity 30.2
Matches 102; Conservative
                                                                                                                                                        476..494
                                                                                                                                                                                                                                                                                                                                                                                                                                       (PURD ) PURDUE RES FOUND.
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N-PSDB; AAX25336.
                                                                     484
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  Key
Misc-difference
                                                                Misc-difference
                                                                                                                                                                                                                             W09902656-A1
                                                                                                                                                                                                                                                                                                                       10-JUL-1998;
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	Matches	102;	Matches 102; Conservative 65; Mismatches 129; Indels	les 129;	Indels	42; Gaps	Gaps	10;	
ø	Qy	26 T	26 TPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSG	IRGALNAVR	SLVPDALER	KPKAVV	THSSG (85	
Д	qa	58 5	58 SPLQLAKKLSKRLGVRMYLKREDLQPVFSFKLRGAYNMWYKLPADQLAKGVICSSAG	: : LRGAYNMWV	KLPADQL	- AKGVI	CSSAG	114	
o	Qy	86 N	NHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPSDESRENVAKRVTEE	AIQAYGASI	VYCEPSDES	RENVAR	RVTEE	145	
Ω	qa	115 N	NHAQGVALSASKLGCTAVIVMPVTTPEIKWQAVENLGATVVLFGDSYDQAQAHAK-IRAE	AVENLGATV	I : VLFGDSYDQ.	: II AQAHAK	I	173	
ø	Qy	146 T	TEGI-MVHPNOEPAVIAGOGTIALEVLNOV-	-PLVDALVV	PVGGGGMLA	GIAITV	KALKP ;	202	
Ω	qa	174 E		GPL-HAIFV	PVGGGGLIA	GIAAYV	I : I	232	
o	٥y	203 s	SVKVYAAEPSNADDCYQSKLKG	IET	ADGVK-SSIGLNTWPIIF	SIGLNI	WPIIR	253	
Д	QQ	233 E	ш	ERVILDQVG	GFADGVAVK	EVGEET	FRISE	283	
ø	Qy	254 D	DLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVKNICIVLS 313	TAGVGVAAV	LSQHFQTVS	PEVKNI	CIVLS	313	٠
Д	qa	284 N	NEMDGVVLVTRDAICASIKDMFEEKRNILEPAGALALAGA-EAYCKYYGLKDVNVVAITS	: : ! AGALALAGA	-EAYCKYYG	LKDVNV	VAITS	342	
Q	Qy	314 G	GGNVDLTSSITWVKQ	ERPASYQ 3	36				
Ω	QQ	343 G	343 GANMNFDKLRIVTELANVGRQQEAVLATLMPEKPGSFK 380	: :: PEKPGSFK 3	80				
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LNAVRSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGV
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Best.Local (
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464.608 Million cell updates/sec
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep;*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep;*
5: /cgn2_6/ptodata/1/iaa/pCTUS_COMB.pep;*
6: /cgn2_6/ptodata/1/iaa/pCTUS_COMB.pep;*
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Compugen Ltd
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US-08-669-378-8
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US-09-789-30A-4
US-09-134-001C-4168
US-09-134-001C-3920
US-09-134-001C-3920
US-09-134-001C-3920
US-09-134-001C-3930
US-09-134-193-13
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   GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
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us-09-889-609b-10.rai

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PRODUCTION OF L-ISOLEUCINE BY MEANS OF RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE DEHYDRATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 RKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYC----E 129
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                                                                                                                                                                                                                                                                                                                                                                                                                       20.1%; Score 348.5; DB 1; 29.9%; Pred. No. 6.7e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                65; Mismatches 137;
                                                                                                                                                                                                                                                                                                                              ORGANISM: Lactococcus lactis subsp. lactis INDIVIDUAL ISOLATE: ILVA
                                         20747/30
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Patent No. 6107063
GENERAL INFORMATION:
APPLICANT: Mocckel, Bettina
APPLICANT: Sahn, Hermann
TITLE OF INVENTION: PECOMBINANT MITTLE OF INVENTION: DEHYDRAPESE:
TITLE OF INVENTION: DEHYDRAPASE
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                    REGISTRATION NUMBER: 30, 727
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                                  REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3000 K Street, N.W.
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Goldman, Michael L.
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                                                                                                    TELEFAX: (716) 263-1487
TELEX: 978450 (WUT)
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                  441 amino acids
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Best Local Similarity 29.9%
Matches 95; Conservative
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HYPOTHETICAL:
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                                                                                                                                                                                                                                           TOPOLOGY:
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APPLICANT: Godon, Jean-Jacques
APPLICANT: Renault, Pierre
TITLE OF INVENTION: Nucleic acid coding for an alpha-acetolactate
TITLE OF INVENTION: synthase from Lactococcus and its applications
                                                                                                    GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
APLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EVIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION UNMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 21.2%; Score 367; DB 4; Length 424; Best Local Similarity 31.1%; Pred. No. 4.8e-33; Matches 100; Conservative 64; Mismatches 142; Indels
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                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR FILING DATE: 1998-08-13

PRIOR PLING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/065,779

PRIOR PLING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

LENGTH: 424
                                         Dequence 3876, Application US/09134001C
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US-09-134-001C-3876
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304 KKQI--ENKTIVCIVSGGNNDI 323
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                    US-09-134-001C-3876
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APPLICANT: Moeckel, Bettina
APPLICANT: Eggeling, Lothar
APPLICANT: Sahm, Hermann
TITLE OF INVENTION: PRODUCTION OF L-ISOLEUCINE BY MEANS OF
TITLE OF INVENTION: RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE
TITLE OF INVENTION: DEHYDRATASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYG---A 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 VK-SSIGLNTWPIIRDLVDDIFTVTEDEIKCATQL--VWERMKLLIEPTAGVGVAAVLSQ 296
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                                                                                                          PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 310.5; DB 3 Pred. No. 1.4e-26;
                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 016881/0142
FELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE95/00017
FILING DATE: 09-JAN-1995
                                                                                                                                                                                                                                                                                           00 926
                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,378
FILING DATE: 20 NAR-1997
                               COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Palace
                                                                                                                                                                                                                                                FILING DATE: 09-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 0(
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-669-378-4; Sequence 4, Application US/08669378; Patent No. 6107063; GENERAL INFORMATION:
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28.1%;
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(202)672-5399
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 17.9 Best Local Similarity 28.1 Matches 94; Conservative
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CORRESPONDENCE ADDRESS:
                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                       CLASSIFICATION:
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27.8%; Pred. No. 1.4e-26;
**ive 61; Mismatches 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 HFQTVSPEVKNICIVLSGGNVDLTSSITWVKQAER 331
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                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 016881/0142
TELECOMMUNICATION INFORMATION:
                                                                                                                                                               DE P 44 00 926.7
                                                                                               APPLICATION NUMBER: PCT/DE95/00017
FILING DATE: 09-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 00 926
FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
CLASSIFICATION: 435
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Patent No. 6107063
GENERAL INFORMATION:
APPLICANT: Mockel, Bettina
APPLICANT: Eggeling, Lothar
APPLICANT: Sahm, Hermann
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                                                                                                                                                                                                                                                                                                              (202)672-5300
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LENGTH: 436 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                             (202)672-5399
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Best Local Similarity 27.89
Matches 93; Conservative
                                                                                                                                                                                                                             NAME: Bent, Stephen A.
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TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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TITLE OF INVENTION: R
TITLE OF INVENTION: D
NUMBER OF SEQUENCES:
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TOPOLOGY:
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Hermann
NE. PRODUCTION OF L-ISOLEUCINE BY MEANS OF
NE. RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE
ON: DEHYDRATASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 309.5; DB 3;
Pred. No. 1.9e-26;
1; Mismatches 160;
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FELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE95/00017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US/08/669,378
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27.8%;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P
FILING DATE: 14-JAN-1994
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                                                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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Best Local Similarity 27.8°
Matches 93; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 904136 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                          CORRESPONDENCE ADDRESS:
      APPLICANT: Sahm, Herm
TITLE OF INVENTION: P
TITLE OF INVENTION: R
TITLE OF INVENTION: D
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
FILING DATE: 20-MAF
                                                                                                                                                                                                                                                CITY: Washington
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20007-5109
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                                                                                                                                                                                                                                                                                   STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 VK-SSIGLNTWPIIRDLVDDIFTVTEDEIKCATQL.-VWERMKLLIEPTAGVGVAAVLSQ 296
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                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | :| :|:||:|||| | : : : |||| | SF---APGSVVVCII-SGGNNDV---LRYAEIAER 344
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3: Foley & Lardner
3000 K Street, N.W., Suite 500
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APPLICATION NUMBER: PCT/DE95/00017
FILING DATE: 09-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 00 926.7
FILING DATE: 14-JAN-1994
ATTORNEY AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/669,378 FILING DATE: 20-MAR-1997 CLASSIFICATION: 435
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Patent No. 6107063
GENERAL INFORMATION:
APPLICANT: Moeckel, Bettina
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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amino acid
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904136
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                                                                                                                                                                                                                                                                      OPERATING SYSTEM:
SOFTWARE: Patentir
                  STREET: SUCC
                                                                                                                    COUNTRY: USA
ZIP: 20007-5109
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ADDRESSEE:
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PRODUCTION OF L-ISOLEUCINE BY MEANS OF RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE DEHYDRATASE
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APPLICATION NUMBER: US/08/669,378 FILING DATE: CLASSIFICATION: 435
297 HFQTVSPEVKNICIVLSGGNVDLTSSITWVKQAER 331
                                    SF---APGSVVVCII-SGGNNDV---LRYAEIAER 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     3: Foley & Lardner
3000 K Street, N.W., Suite 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                         ; Sequence 8, Application US/08669378
; Patent No. 6107063
                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Mocckel, Bettina
APPLICANT: Eggeling, Lothar
APPLICANT: Sahm, Herman
TITLE OF INVENTION: RECOMICAN
TITLE OF INVENTION: BETOMETA
TITLE OF INVENTION: BETOMETA
TITLE OF SEQUENCES: 18
NUMBER OF SEQUENCES: 18
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 09-JAN-1995
PRIOR APPLICATION NUMBER:
FILING DATE: 14-JAN-1994
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COMPUTER READABLE FORM: TYPE: Floppy disk
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(202)672-5399
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ATTORNEY/AGENT INFORMATION:
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Best Local Similarity 28.6
Matches 96; Conservative
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                    PRODUCTION OF L-ISOLEUCINE BY MEANS OF
RECOMBINANT MICROORGANISMS WITH DEREGULATED THREONINE
DEHYDRATASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 AEVKRVGDLNYTIVEKNQGRVHMMSATEGAVCTEMLDLYQNEGIIAEPAGALSIAGLKEM 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYG---A 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 GAQSPQEQRDAGIVAASAGNHAQGVAYVCKSLGVQGRIYVPVQTPKQKRDRIMVHGGEFV 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7 ISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/669,378 FILING DATE: CLASSIFICATION: 435 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.8%; Score 309.5; DB 3; 27.8%; Pred. No. 1.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Mismatches 160;
                                                                                                                                                                                                                                                                 Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 016881/0142 FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DE P 44 00 926.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/DE95/00017
FILING DATE: 09-740-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 00 926.
                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
            Sequence 10, Application US/08669378 Patent No. 6107063
                                                                                                                                                                                                                                           ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                APPLICANT: Eggeling, Lothar APPLICANT: Sahm, Hermann
                                                                             APPLICANT: Moeckel, Bettina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 14-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (202)672-5300
(202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      436 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Bent, Stephen A. REGISTRATION NUMBER: 2
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                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                    Washington
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Matches 93; Conserv
                                                                                                                                                                                                                                                                                                                                                20007-5109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                         D.C.
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COUNTRY:
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198 VMVPVGGGGLLAGVVSYMADMAPRTAIVGIEPAGAAS-MQAALHNGGPITLETVDPFVDG 256
                                     --VKSSIGLNTWPIIRDLVDDIFTVTEDEIKCATQL--VWERMKLLIEPTAGVGVAAVLS 295
                                                                           257 GEVKRVGDLN-YTIVEKNQGRVHMMSATEGAVCTEMLDLYQNEGIIAEPAGALSIAGLKE 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----RSLVPDALERKPK-AVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLA- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 KLGKKGGIVPGTVQVESKTTIIEPTSGNTGIALALAAALLGLKCTIVMPATDTSREKRAQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 LRALGAELVVVPVAGGGSDDLADAIAKAEE--LAEENPENAYLLNQAAGPFDNPANPEIA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        205 KVYAAEPSNADDCYQSKLKGKLMPNLY-------PPETIADGVKSSIG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----IA 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 LN-----TWPIIRDL-----VDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAA 292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19 IRDSIHLTPVLTSSILNQLTGRNL-----FFKCE-LFQKTGSFKIRG-ALNAV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 VTELIGNIPLVRLNRLSKELGEGLGANAAVEIYLKLEDLNGPIGSFKDRGLALNMILLAE
                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Weavers, Rachel
APPLICANT: Rudolph-Owen, Laura A.
TITLE OF INVENTION: 22406, A No. 6458576el Human Pyridoxal-Phosphate
TITLE OF INVENTION: Dependent Enzyme Family Member and Uses Therefore
FILE REFERENCE: 35800/20899, 300A
CURRENT APPLICATION NUMBER: US/09/789, 300A
PRIOR APPLICATION NUMBER: US 60/183, 208
PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Pyridoxal-Phosphate Dependent Enzyme Family Domain OTHER INFORMATION: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 378;
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es 126;
                                                                                                                     296 QHFQTVSPEVKNICIVLSGGNVDLTSSITWVKQAER 331
                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.3%; Score 283.5;
ilarity 28.3%; Pred. No. 1.4c
Conservative 55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     293 VLSQHFQTVSP--EVKNICIVLSGG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         354 ALKLAKEGKKPLNKGKTIVVILSGG 378
                                                                                                                                                                                                                                                              Sequence 4, Application US/09789300A
Patent No. 6458576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                        RESULT 10
US-09-789-300A-4
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Sequence 1, Application US/09088435 Patent No. 6277619

.09-088-435-1

RESULT 11

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58 EMAKKGCRHLVCSSGGNAGIAAAYAARKLGIPATIVLPESTSLOVVORLOGEGAEVOLTG 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                182 VPVGGGGMLAGIAITVKAL----KPSVKVYAAEPSNADDCYQSKL-KGKLMPNLYPPETI 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 AD--GVKSSIGLNT------WPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIE 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 -VYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALE---VLNQVPLVDALV 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 PDITSVAKSLGAKTVAARALECMQVCKIHSEVVEDTEAVS-----AVQQLLDDERMLVE 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 ADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AKQEPFHV-----VTPLLESWALSQVAGMPVFLKCENVQPSGSFKIRG----IGHFCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70 DALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   284 PTAGVGVAAVLS-----QHFQTVSPEVKNICIVLSGGN 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113;
                                      GUEGLER, KARL J.
PATTERSON, CHANDRA
FONTION: SERINE DEHYDRATASE HOMOLOG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 259.5; DB 4
Pred. No. 5.8e-21;
                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PF-0512 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                         3: Incyte Pharmaceuticals,
3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/088,435 FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15.0%;
28.6%;
  LAL, PREETI
CORLEY, NEIL C.
                                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : 325 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Cerrone, Michael REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
PREETI
                                                                              TITLE OF INVENTION: SE
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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Best Local Similarity
                                                                                                                                                            STREET: 3174 Por CITY: 'Palo Alto
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2752518
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMMEDIATE SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                           ADDRESSEE:
                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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84 SGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCE-----PSDESRENV 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 KLKEKCPGCRIIGVDP------EGSI----LAEPEELNQTEQTTYEVEGIGYDFIP 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 AWRLKNEIPNSHILDOYRNASNPLAHYDTTADEILQOCDGKLDMLVASVGTGGTITGIAR 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          251 II--RDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAG--VGVAAVLSQHFQTVSPEVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 TPVLTSSILNQLTGR--NLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKAVVTHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 TVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSS----IGLNTWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 TPVLTSSILNQLTGR--NLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKAVVTHS
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APPLICANT: Yuan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.8%; Score 187; DB 4; Length 551; 25.2%; Pred. No. 2.7e-12;
                                                                                                                                                                                                                                                                                                                                                                                                           Length 551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----DLTSSITW 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368 QRCVVILPDSVRNYMTKFLSDRWMLQKGFLKEEDLTEKKPW 408
                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 187; DB 1; I; Pred. No. 2.7e-12; 46; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
              IMBER: US/08/120,960
12-SEP-1993
                                                                                                         NAME: PEPPER PH.D., FREDERICK W. RELECOMMUSICATION NUMBER: 31,286
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/09347878C Patent No. 6376210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      46;
                                                                                                                                                                                                                                                                                                                                                                                                         10.8%;
25.2%;
                                                                                                                                                                                               TELEFAX: 619-453-2839
INFORMATION FOR SEQ ID NO: 2:
                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        551 amino acids
                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 25.2%
Matches 86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 75
SOFTWARE: PatentIn Ver. 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: protein US-08-120-960-2
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                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                           amino acid
                                                                                                                                                                                                                                                                                                                linear
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                                          FILING DATE: 12 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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US-09-347-878-9
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Best Local 9
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                                                                                                    GENERAL INFORMATION:
APPLICANT: LYDID DOUGETEE-Stamm et al
APPLICANT: LYDID DOUGETE ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 LVDD----IFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVKNICI 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86 N-HGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQA--YGASIVYCEPSDESRENVAKRV 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143 TEETEGIMVHPNQEPAVIAGGGTIALEVLNQV--PLVDALVVPVGGGGMLAG----IAI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 TVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSSIG-LNTWPIIRD 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218 HNKKNTOLPOMFGFQAEGASPIVONKI-----IKNPETIATAIR--IGNPASWOKAVN 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 TPLIYCENLSOKLDIELYVKYEGANPTGSFKDRGMVMAVTK----AKEQGKKVVICASTG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26 TPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: DILWORTH & BARRESE
STREET: 4350 LA JOLLA VILLAGE DRIVE, SUITE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 13.9%; Score 241.5; DB 4; Best Local Similarity 28.1%; Pred. No. 8.1e-19; Matches 93; Conservative 58; Mismatches 149;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: KRAUS, JAN P
TITLE OF INVENTION: DNA SEQUENCE ENCODING HUMAN
TITLE OF INVENTION: CYSTATHIONINE B-SYNTHASE
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              311 VLSG-GNVDLTSSITWVKQAERPASYQSVSV 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          329 ILTGNGLKDPDTAISLLDNPIQPLPNNKESI 359
                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PELING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                            Sequence 4168, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Palace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/08120960 Patent No. 5523225 GENERAL INFORMATION:
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                RESULT 12
US-09-134-001C-4168
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LENGTH: 367
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Job time : 24.5317 secs
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CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 312
                                                                                                                    TVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSS----IGLNTWP 250
                                                                                     AKRVTEE--TEGIMVHPNQEPAVIAGQGTIALEVLNQVP-LVDALVVPVGGGGMLAGIAI 195
                                                                                                                                                                                                                          ----EGSI---LAEPEELNQTEQTTYEVEGIGYDFIP 312
  SGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCE-----PSDESRENV 138
                                                                                                                                                                                                                                                                    251 II -- RDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAG--VGVAAVLSQHFQTVSPEVK 306
                                                                                                                                                                                                                                                                                               : | :| | :: | :: | :: | :| 313 TVLDRTVVDKWFKSNDEBAFTFARMLIAQEGLLCGGSAGSTVAVAVVAAQELQE-----G 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79 VVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPSDESRENV 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 --RRIPKAEG-MIGAQQEALAYATRYGYLYMNQFETKDNPGAYTQTLAKQLIDELSHIDY 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 FVAGVGSGGTFTGVAQHLKTY--DVKNYIVEPEG-----SVLNGGVS---HPHAT---- 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----GTIALEVLNQVPLVDA 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 VKSSIGLNTWP--IIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQH 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 DSIHLTPVLTSSILNQLTGRN--LFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPKA 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15 DLIGOTPLV --- LLESFSDENVKIYAKLEQFNPGGSIKDRLGKYLIEKAIDEGRLKEGDT
                                         147 SGNTGIGLALAAAVRGYRCIIVMPEKMSSEKVDVLRALGAEIVRTPTNARFDSPESHVGV
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                                                                                                                                                                                                                                                                                                                                                                                        Query Match 10.0%; Score 174; DB 4; L. Best Local Similarity 23.6%; Pred. No. 3.1e-11; Matches 74; Conservative 48; Mismatches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 AKRVTEETEGIMVHPNQEPAVIAGQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 09-134-001C-3920.
Sequence 3920, Application US/09134001C
Patent No. 6380370
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/cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              417779 seqs, 108206813 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                   OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Maximum DB seq
                                                                                                                                                                                                                                                                                      Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		æ			CHANGE	
Result No.	Score	Query	Query Match Length DB	DB	ID	Description
-	349.5	20.1	310	6	US-09-738-626-4591	Sequence 4591, Ap
7	311.5	18.0	436	6	US-09-738-626-5828	Sequence 5828, Ap
e	192.5	11.1	306	10	US-09-815-242-13657	Sequence 13657, A
₹7	190.5	11.0	308	6	US-09-738-626-6317	Sequence 6317, Ap
5	174.5	10.1	310	10	US-09-815-242-10707	Sequence 10707, A
9	169.5	9.6	313	10	US-09-815-242-12146	Sequence 12146, A
7	169.5	9.6	313	10	US-09-815-242-12800	Sequence 12800, A
8	169.5	9.6	323	10	US-09-815-242-10239	Sequence 10239, A
6	167.5	9.7	303	10	US-09-815-242-5437	Sequence 5437, Ap
10	161.5	9.3	323	10	US-09-815-242-13862	Sequence 13862, A
11	154	8.9	383	6	US-09-931-457A-65	Sequence 65, Appl
12	149	9.8	314	10	US-09-815-242-5737	Sequence 5737, Ap
13	148	8.5	325	6	US-09-931-457A-32	Sequence 32, Appl
14	147	8.5	324	σ	US-09-905-290A-4	Sequence 4, Appli
15	147	8.5	386	6	US-09-931-457A-66	Sequence 66, Appl
16	147	8.5	398	σ	US-09-931-457A-62	Sequence 62, Appl
17	146	8.4	415	6	US-09-931-457A-64	Sequence 64, Appl
18	143.5	8.3	316	10	US-09-815-242-11179	Π
19	143.5	8.3	324	10	US-09-815-242-11879	Sequence 11879, A

Sequence 31, Appl Sequence 11292, A Sequence 5838, Ap Sequence 22, Appl Sequence 22, Appl Sequence 25, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl Sequence 28, Appl Sequence 28, Appl Sequence 120, Appl Sequence 120, Appl Sequence 154, Appl Sequence 154, Appl Sequence 155, Appl Sequence 15, Appl Sequence 16, Appl Sequence 113, Appl Appl Sequence 113, Appl Appl Sequence 113, Appl Sequence 113, Appl Appl Sequence 113, Appl Appl Appl Appl Appl Appl Appl App	Sequence 13897, A
9 US-09-931-457A-31 0 US-09-815-242-11292 10 US-09-815-242-11292 10 US-09-815-242-11635 10 US-09-935-211A-4 9 US-09-742-096-22 9 US-09-742-096-5 10 US-09-742-096-5 10 US-09-742-096-5 10 US-09-742-096-5 10 US-09-742-096-5 10 US-09-742-096-5 10 US-09-742-096-5 10 US-09-742-10286 10 US-09-815-242-11335 10 US-09-815-242-10286 10 US-09-915-242-10286 10 US-09-915-242-10286 10 US-09-915-242-10286 10 US-09-915-242-10286 10 US-09-915-242-10286 10 US-09-915-242-10286 10 US-09-915-242-10286 10 US-09-915-242-10386 10 US-09-915-242-10386 10 US-09-928-457-40	10 US-09-815-242-13897
325 306 317 250 1187 1786 630 212 630 1643 472 472 473 473 474 474 474 474 474 857 877 877 877 877 877 877 877 877 877	319
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139 1115.20 1115.20 1112.105 1001.5 1001.5 1001.5 95.5 95.5 95.5 93.9 93.9 93.9 93.9 93	87.5
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ALIGNMENTS

7 ISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRS 66 Length 310; Indels 20.1%; Score 349.5; DB 9; 29.1%; Pred. No. 8.2e-25; tive 55; Mismatches 146; APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: NAKAGAWA, SATOSHI
APPLICANT: MIZOGUCHI, HIROSHI
APPLICANT: ANDO, SEIKO
APPLICANT: O'CHIAI, MIKIRO
APPLICANT: TOKOI, HARUHIKO
APPLICANT: TOKOI, HARUHIKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: SENOH, AKIHIRO
APPLICANT: O'SAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18 PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SCFTWARE: Patentin ver. 3.0
LENGTH: 310 Sequence 4591, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION: ; TYPE: PRT ; ORGANISM: Corynebacterium glutamicum US-09-738-626-4591 Query Match 20.1% Best Local Similarity 29.1% Matches 95; Conservative

67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV 126

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257 AAVKRVGDLNYTIVEKNOGRVHMMSATEGAVCTEMLDLYQNEGIIAEPAGALSIAGLKEM 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| :||| | |: : :| |||| |: : 6 TIVEATSGNTGIGLSWVGAAKGYKVVIVMPETMSVERRKIIQAYGAELVLTPGSEGMKGA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 VGGGGMLAGIALTVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADG-VKS, 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78 AVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPSDESREN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 VAK--RVTEETEGIMVHPNQEPA-----VIAGQGTIALEVLNQVPLVDALVVP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18 NIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALERKPK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               231 TLDTKAY-----GISSAAAI 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes TITLE OF INVENTION: Prokaryotes FILE REFERENCE: ELITRA.011A CURRENT APPLICATION NUMBER: US/09/815,242 CURRENT FILING DATE: 2001-03-21 PRIOR APPLICATION NUMBER: 60/191,078 PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.1%; Score 192.5; DB 10; 24.0%; Pred. No. 5.5e-10; ive 57; Mismatches 124;
                                                                                                                | :| :| :| :| || || || SF---APGSVVVCII-SGGNNDV---LRYAEIAER 344
                                                                                     297 HFQTVSPEVKNICIVLSGGNVDLTSSITWVKQAER 331
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13657
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PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PELING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                          Sequence 13657, Application US/09815242 Patent No. US20020061569A1
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PRIOR FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamamoto, Robert T
                                                                                                                                                                                                                                                                                                                               Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
                                                                                                                                                                                                                                                                                                                                                                        Wall, Daniel
Trawick, John D.
Carr, Grant J.
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Best Local S
Matches 70
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187 GGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKS-SIG 245
                                                                                                                                                                           127 YCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGG 186
                                                                                          |: || :| || || || OIGSEYAEAFEAAQTFESETGALFCHAYDQPDIAAGAGVIGLEIVEDLPDVDTIVVAVGG 178
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                                                                                                                                                                                                                                     ------LNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVL 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 18.0%; Score 311.5; DB 9; Best Local Similarity 27.8%; Pred. No. 5.3e-21; Matches 93; Conservative 61; Mismatches 160;
                                                                                                                                                                                                                                                                                                                             SQHFQTVSPEVKNICIVLSGGNVDLTS 321
                                                                                                                                                                                                                                                                                                                                                        SGAYKPAADE--KVAVIVCGANTDLTT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5828, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIZOGUCHI, HIROSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: NAKAGAWA, SATOSHI
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SOFTWARE: Patentin ver. 3.0
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128 IAKATALAEEHGYFMPLQFNNPANPMIHEQKTGKEIVDVFGKRGL-DAFVSGVGTGGTVT 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 VAK--RVTEETEGIMVHPNQEPA--VIAGQ--GTIALEVLNQVPLVDALVVPVGGGGMLA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 GIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSSIGLNTWPI 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATELIGOSPVVKLKRMVPEGAADVFVKLEFFNPGGSVKDRIALSMIQQAEADGRLKPGQ 67
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                                       APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                 FILE REFERENCE: ELITRA 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                      PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/191, 078
PRIOR APPLICATION NUMBER: 60/206, 848
PRIOR PELING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207, 727
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR PELICATION NUMBER: 60/253, 625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR APPLICATION NUMBER: 60/257, 931
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2001-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecalis
                                                                                                                                                                         2001-03-21
                       Yamamoto, Robert T.
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Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
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Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68; Conservative
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Carr, Grant J
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| :||| | || || 64 TIVEATSGNTGIALAMYGAARGYNVVLTMPETMSNERRYVLLRAYGAEIVLTPGAAGMQGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        131 SDESRENVAKRVTEETEGIMVHPNQEPAVIAGQ------GTIALEVLNQVP-LVD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 KDKADEIVAER------ENAVLARQFENEANPRVHRDTTAKEILEDTDGNVD 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         179 ALVVPVGGGMLAGIAITVKALKPSVKVYAAEPS-----NADDCYQSKLKGKLMPNLYPP 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 234 ETIADGVKSSIGLNTWPII--RDLVDDIFTVT-EDEIKCATQLVWERMKLLIEPTAGVGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 308;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%; Score 190.5; DB 9; 25.7%; Pred. No. 8.5e-10; Live 40; Mismatches 125;
                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Corynebacterium glutamicum US-09-738-626-6317
                                                                  Sequence 6317, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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ANDO, SEIKO
                                                                                                                                                                                                              APPLICANT: HAYASHI, MIKIRO
APPLICANT: OCHIAI, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: SENOH, AKIHIRO
APPLICANT: IKEDA, MASATO
APPLICANT: OZAKI, AKIO
                                                                                                                                              APPLICANT: NAKAGAWA, SATOSHI
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SOFTWARE: PatentIn ver. 3.0
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Matches 78; Conservative
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                                       US-09-738-626-6317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 TPGSEAMKGAIKKAKELKEEHGYF-EPQQFENPANPEV--HELTTGPELLQQFEGKTIDA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 LVVPVGGGMLAGIAITVKALKPSVKVYAAEPS-----NADDCYQSKLKGKLMPNLYPPE 234
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-03-21
   PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PAPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-12-22
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
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PRIOR APPLICATION NUMBER: 60/207,727
                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Staphylococcus aureus US-09-815-242-12800
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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APPLICANT:
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APPLICANT: Carr, Grant J.
APPLICANT: Carr, Grant J.
APPLICANT: Xu, H. Howard
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in FITLE PEFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.8%; Score 169.5; DB 10; 24.5%; Pred. No. 8.4e-08; ative 50; Mismatches 143;
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                        PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PELING DATE: 2000-11-27
PRIOR PAPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR PELICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2000-12-22
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Patent No. US20020061569A1
PENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
60/191,078
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Zyskind, Judith W.
Wall, Daniel
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Best Local Similarity 24.5%
Matches 74; Conservative
   APPLICATION NUMBER:
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US-09-815-242-12800
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138 VAKRVTE--ETEGIMVHPNQ-----EPAVIAGQGTIALEVLNQV--PLVDALVVPVGGGG 188
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                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                       ; Score 167.5; DB 10; Length
; Pred. No. 1.2e-07;
49; Mismatches 137; Indels
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FASLSEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-12-22
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PRIOR FILING DATE: 2000-03-21
                                                                                                                                                                              ORGANISM: Staphylococcus aureus
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Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
Carr, Grant J.
Yamamoto, Robert T.
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Best Local Similarity 24.6%;
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ORGANISM: Salmonella typhi
                                                                                                                                                                                                                                                                                                             72; Conservative
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LENGTH: 323
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 TPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALER---KPKA-VVT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41;
                                                                                                                                                                                                                                                                                                                                                                DB 10; Length 323;
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TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                           9.8%; Score 169.5; DB ]
ilarity 24.5%; Pred. No. 8.8e-08;
Conservative 63; Mismatches 136
          PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10239
LENGTH: 323
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
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APPLICATION NUMBER: 60/253,625
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Yamamoto, Robert T.
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Wall, Daniel
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Best Local Similarity
Matches 78; Conserv
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AEPSNADDCYQSKLKGKLMPNLYPPETIADG-VKSSIGLNTWPIIRDLVDDIFTVTEDE- 266
                                                                                                                                                                                              267 IEPT-----ESNILSGGKPGPHKIQGLGAGFVPSNLDLG------VMDEVIEVSSEEA 313
                                                                 VHPNQEPA-VIAGQGTIALEVLNQVP-LVDALVVPVGGGGMLAGIAITVKALKPSVKVYA 208
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21.9%; Pred. No. 7.3e-06;
tive 62; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of Essential Genes in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Identification of Essenti
FILE REFERENCE: ELITRA 011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT ELING DATE: 2001-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-33
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-110-23
PRIOR FILING DATE: 2000-11-27
PRIOR PRIOR DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
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OTHER INFORMATION: Xaa = Any Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5737, Application US/09815242
Patent No. US20020061569A1
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APPLICATION NUMBER: 60/269,308
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Zyskind, Judith W.
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Trawick, John D.
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NUMBER OF SEQ ID NOS: 14110
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Best Local Similarity
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                                                                                                                                                                                                                26 TPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALER----KPKA-VVT
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                                                                                                                                                                         65;
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                                                                                                                              Length 323;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Allen, Stephen M.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
FILE REFERENCE: BB1116 US CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 CISFADVEKAHINIRDSIHLTPVLTSSILN-----QLTGR-
                                                                                                                          ; Score 161.5; DB 10;
; Pred. No. 5e-07;
63; Mismatches 126; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
8.9%; Score 154; DB 9; L
Best Local Similarity 22.9%; Pred. No. 3.3e-06;
Matches 75; Conservative 59; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 KLQ-EDESFTNKNIVVILPSSGERYLSTAL 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT PEDLICATION NUMBER: US/09/931,457A
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/424,976
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/065,385
PRIOR APPLICATION NUMBER: 60/065,486
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/049,406
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        295 SQHFQTVSPEVKNICIVL-SGGNVDLTSSI 323
                           : LOCATION: (1)...(323)
; OTHER INFORMATION: Xaa = Any Amino Acid US-09-815-242-13862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 65, Application US/09931457A Patent No. US20020157132A1 GENERAL INFORMATION:
                                                                                                                          9.3%;
                                                                                                                        Query Match
Best Local Similarity 23.0%
Matches 76; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Falco, S. Carl
                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -09-931-457A-65
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                  NAME/KEY:
LOCATION:
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g à а à 요 δ g

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APPLICANT: Nye, Gordon
TITLE OF INVENTION: METHODS FOR MEASURING CYSTEINE AND DETERMINING CYSTEINE SYNTHA
FILE REPERBENCE: Docket No. US20030087327A12090US
CURRENT APPLICATION NUMBER: US/09/905,290A
CURRENT FILING DATE: 2001-07-13
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                   13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 LVPDALERKPKA-VVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASI 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 VYCEPS-----DESRENVAKRVTEETEGIMVHPNQEPA-------VIAGQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 GTIALEVLNQVPLVDALVVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLK 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------VDILVAGVGTGGTLSGSGRFLKEKNKDFKVYGVEPT-----ESAVI 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 GKLMPNLYPPETIADG-VKSSIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLI 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 VEKAHINIRDS----IHLTP-VLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 SFADVEKAHI--NIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVR 65
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                                                                                                                                                                                                                                                                                                                                                                                                   70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 GISSGAAAAAAIK----VAKRPENAGKLIVVIFPSGGERYLSTSL 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     283 EPTAGVGVAAVLSQHFQTVSPEVKN----ICIVLSGGNVDLTSSI 323
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APPLICANT: Falco, Stephen M.
TITLE OF INVENTION: Plant Amino Acid Biosynthetic Enzymes
TILE REFERENCE: BB1116 US CIP
CURRENT APPLICATION NUMBER: US/09/931,457A
CURRENT FILING DATE: 2002-02-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.5%; Score 147; DB 9; L
19.2%; Pred. No. 1.5e-05;
iive 60; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                  ; DB 9;
1.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                62; Mismatches
                                                                                                                                                                                                                                                                                                                                                  8.5%; Score 147; 22.3%; Pred. No. 1
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/065,385
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/049,406
PRIOR FILING DATE: 1997-06-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 66, Application US/09931457A Patent No. US20020157132A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      ORGANISM: Arabidopsis thaliana US-09-905-290A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 72
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : Solanum tuberosum
                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 22.39 Matches 77; Conservative
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Best Local Similarity 19.2%
Matches 64; Conservative
  Crawford, John
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ORGANISM:
                                                                                                                                                                                                   SEQ ID NO 4
                                                                                                                                                                                                                                                    TYPE: PRT
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STTGSIMGMSRKIKEVHPNAQIIAVD--------AKGSV 206
                                                                                                                                                                   245 GLNTWPIIRDL------VDDIFTVTEDEIK----CATQLVWERMKLLIEPTAGVG 289
                                                                                                                                                                                                     207 IFGDKPINRELPGIGASRVPRNIEXIRNXSSDPCRXLSICFGLSKTDXLXRHICGGSTGS 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 GIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPS-----DESRENVAK------ 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 -----RVTEETEGIMVHPNQEPAVIAGGGTIALEVLNQVPLVDALVVPVGGGGMLAGIAI 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 NPANPKIHYETTG------PEIWRGSG------GKIDALVSGIGTGGTVTGAGK 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 TVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-----SSIGLNTW 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38 KLEMMEPCSSVKDRIGY----SMISDA-ENKGLITPGESVLIEPTSGNTGIGLAFIAAAK 92
                                                                   185 GGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45 KCELFQKTGSFKIRGALNAVRSLVPDALERK-----PKAVVTHSSGNHGQALTYAAKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---AILSGGKPGPHKIQGIGAGFI
                                                                                                                                                                                                                                                                    290 VAAVLSQHFQTVSPEVKNICIVLSGGN--VDLTSSITWVKQAERPASYQSV 338
                                                                                                                                                                                                                                                                                                267 IIAAIEQLITSIEEGATIVTILPDRGDRYLDLVYSDTWL---EKMKSROGV 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 235 PGVLDVNLLDEVIQVSSEESIETAKLLALKEGLLVGISSGAAAAAI 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
TITLE OF INVENTION: Plant anno Acid Biosynthetic Enzymes
FILE REFERENCE: Bell16 US CIP
CURRENT FILING DATE: 2002-02.
PRIOR FILING DATE: 199-12-02
PRIOR FILING DATE: 199-12-02
PRIOR FILING DATE: 199-11-12
PRIOR APPLICATION NUMBER: 60/065,385
PRIOR APPLICATION NUMBER: 60/065,385
PRIOR APPLICATION NUMBER: 60/049,406
PRIOR FILING DATE: 1997-06-12
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 72
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 325,
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Pred. No. 9.5e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32, Application US/09931457A Patent No. US20020157132A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 YLKEQNPNIKLYGVEPVES----
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US-09-905-290A-4
US-09-905-290A-4
Sequence 4, Application US/09905290A
Publication No. US20030087327A1
GENERAL INFORMATION:
APPLICANT: Rice, John
; APPLICANT: Lanning, Beth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Citrullus lanatus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64; Conservative
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Matches

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qq	60 SSTEIEGLNIAEDVTQLIGNTPMVXLNTIAKGCVANIAAKLEIMEPCCSVKDRIGF 115
Qy	Æ
qq	116 SMIVDAEEKGLISPGKTVLVEPTSGNTGIGLAFIAASRGYKLILTMPASMSLERRVILKA 175
Οy	RVTEETEGIMVHPNQEPAVIAGQGTI
qq	176 FGAELVLTDPAKGMKGAVSKAEEILNNTPDAYIL 209
Οy	176TVDALVVPVGGGMLAGIAITVKALKPSVKVYAA 209
qq	210 QQFDNPANPKIHYETTGPEIWEDTKGKIDILVAGIGTGGTITGTGRFLKEQNPNIKIIGV 269
Qy	210 EPSNADDCYQSKLKGKLMPNLYPPETIADGVKSSIGLNTWPIIRDLVDDIFT 261
qq	270 EPTESNVLSGGKPGPHKIQGIGAGFIPGNLDQDVMDEVIE 309
ΟŸ	262 VTEDE-IKCATQLVWERMKLLIEPTAGVGVAAVL 294
qa	310 ISSDEAVETARTLALQE-GLLVGISSGAAALAAI 342
Search	Search completed: June 24, 2003, 06:16:50

Job time : 277.907 secs

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GenCore version 5.1.6
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- protein search, using sw model OM protein June 24, 2003, 06:07:29 ; Search time 27.0398 Seconds Run on:

(without alignments)
1208.801 Million cell updates/sec

US-09-889-609B-10 1735 1 MCAQYCISFADVEKAHINIR......SSITWVKQAERPASYQSVSV 340

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues Searched:

283224

seq length: 0 seq length: 200000000 Minimum DB : Maximum DB :

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

1 802.5 2 605 3 565 4 4 536 4 4 535 7 517.5 10 496.5 11 496.5 12 461.5 13 471.5 14 471.5 16 471.5 17 471.5 18 461.5 19 461.5	2000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	6 4 6 4 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	000000000000000000000000000000000000000	T04211 744211 741297 E83310 F36434 D72386 F89921 T24337 AF2912 A87687 AF2912 B90166 G87633 AB0897 AG0496 AG0496 D85778	probable threonine threonine ammoniathreonine ammoniathreonine ammoniathreonine ammoniathreonine ammoniathreonine ammoniathreonine ammoniathreonine ammoniathreonine dehydratthreonine ammoniathreonine
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RESULT S38061

ammonia-	dehydrat	threonine	dehydrat	ammonia-	ammonia-	ammonia-	ammonia-	ammonia-	dehydrat	ammonia-	dehydrat	ammonia-	ammonia-	dehydrat	ammonia-
threonine ammonia	threonine	probable	threonine	threonine ammonia-	threonine ammonia	threonine ammonia	threonine ammonia-	threonine	threonine	threonine	threonine	threonine ammonia.	threonine	threonine	threonine
					₹#	₹7	•		•	•					7
877559	A87700	C72630	B83479	DWBYT	AG047	E8237	A6964	AI2334	AF183	T51712	AH1694	A38628	AB0924	AG1323	B9121
2 877559	2 A87700	2 C72630	2 B83479	1 DWBYT	2 AG047	2 E8237	2 A6964	2 AI233	2 AF1839	2 T51712	2 AH1694	2 A38628	2 AB0924	2 AG1323	2 B9121
508 2 877559	C)	~	~	-	N	7	7	7	~	7	7	~	2	7 7	2 E
7	400 2	349 2	515 2	576 1	514 2	510 2	422 2	503 2	257 2	592 2	422 2	595 2	514 2	422 2 P	514 2 E
508 2	24.0 400 2	24.0 349 2	23.2 515 2	22.5 576 1	22.2 514 2	22.1 510 2	21.8 422 2	21.7 503 2	21.4 257 2	21.2 592 2	21.0 422 2	20.9 595 2	20.9 514 2	20.8 422 2 #	20.8 514 2 E

ALIGNMENTS

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probable threonine ammonia-lyase (EC 4.3.1.19) T5C23.70 [similarity] - Arabidopsis th C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jun-2002
C;Accession: T04.21!
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancro submitted to the Protein Sequence Database, March 1999
A;Reference number: Z15261
                                                                                                                                                                                                                                                                                                               A.Map position: 4
A.Introns: 55/2: 99/2: 176/2: 263/2
A.Note: 75/23: 70
C.Superfamily: threonine dehydratase
C.Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 TAPDCKKLAIQAYGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIAL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EVLNQVPLVDALVVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMP 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-346 <BEV>
A;Cross-references: EMBL:AL049500
A;Experimental source: cultivar Columbia; BAC clone T5C23
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 46.3%; Score 802.5; DB 2; Best Local Similarity 48.5%; Pred. No. 1.1e-54; Matches 163; Conservative 67; Mismatches 83;
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H.; Wambutt,

Wedler,

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A;Accession: T41325
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1.323 cGWI>
A;Residues: 1.323 cGWI>
A;Cross-references: EMBL:AL031603; PIDN:CAA20920.1; GSPDB:GN00068; SPDB:SPCC330.15c
             R;Gwilliam, R.; Barrell, B.G.; Rajandream, M.A.; We
Submitted to the EMBL Data Library, September 1998
A;Reference number: 221987
A;Accession: T41325
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NKRIGIIISGGNVDI 314
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Matches 127, Conservative
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nes 119; Conserv
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A; Residues: 1-320 <STO>
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threonine ammonia-lyase (EC 4.3.1.19) YKL218c [similarity] - yeast (Saccharomyces cerevial Nathernate names: protein D336 C.5pecies: Saccharomyces cerevisiae C.5apecies: Sample S44320 C.Accession: S38061; S44320 R.7Alexandraki, D.7 Termia, M. Sequence Database, March 1994 A.Accession: S38061 S48064 A.Accession: S38064 A.Accession: S38064 A.Accession: S38064 A.Accession: S38064 A.Accession: S38064 A.Accession: S38064 A.Accession: S4806 A.Accession: S48130 A.Accession: 
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Threonine ammonia-lyase (EC 4.3.1.19) SPCC320.14 [similarity] - fission yeast (Schizosac threonine ammonia-lyase (EC 4.3.1.19) SPCC320.14 [similarity] - fission yeast (Schizosac C; Species: Schizosaccharonyees pombe
C; Species: Schizosaccharonyees pombe
C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jun-2002
C; Accession: T41297; T41325
R; Wood, V.; Rajandream, M.A.; Barrell, B.G.; Wedler, H.; Wambutt, R.; Wedler, E.
Submitted to the EMBL Data Library, March 1998
A; Reference number: 221986
A; Accession: T41297
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Astatus: preliminary
A; Astatus: A; Awoo
A; Kestidues: 1-323 - wwoo
A; Cross-references: EMBL:AL022245; PIDN:CAA18316.1; GSPDB:GN00068; SPDB:SPCC320.14
A; Experimental source: strain 972h-; cosmid c320
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Matches 133; Conservative
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L-serine ammonia-lyase (EC 4.3.1.17) [similarity] - Pseudomonas aeruginosa (strain PA C; Species: Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa C; Species: Pseudomonas aeruginosa C; Species: Sep-2000 #sequence_revision 15-Sep-2000 #text_change 21-Jun-2002 C; Accession: E83310 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; adman, X.; Pan, Y.; Ebrody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L. L. Lory, S.; Olson, M.V.
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A;Reference number: A82950; MUID:20437337; PMID:10984043
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                                                                                         A;Map position: 3
C;Superfamily: threonine dehydratase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase
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C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase
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                                                                                                                                                                                                                      32.6%; Score 565; DB 2; 40.3%; Pred. No. 2.7e-36;
A;Experimental source: strain 972h-; cosmid c330
C;Genetics:
A;Gene: SPCC320.14; SPCC330.15c
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threonine ammonia-lyase (EC 4.3.1.19) TM0356 [similarity]
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292 KGKKVAIVISGGNIDV 307
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Best Local Similarity
Matches 119; Conserva
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A;Molecule type: DNA
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A; Residues: 1-346 <K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         threonine ammonia-lyase (EC 4.3.1.19) SCF43A.11c [similarity] - Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: Streptomyces coelicolor C; Species: 136434 R; Seeger K; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. Submitted to the EMBL Data Library, July 1999 A; Reference number: 221598 A; Accession: T36434 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Residues: 1-325 <-SEE> A; Residues: 1-325 <-SEE> A; Residues: 1-325 <-SEE> A; Cross-references: EMBL:AL096837; PIDN:CAB48898.1; GSPDB:GN00070; SCOEDB:SCF43A.11c C; Genetics: Screin A3(2) C; Genetics: Screin A3(2) C; Genetics: Screin Generics: C; Superfamily: threonine dehydratase C; Superfamily: threonine dehydratase C; Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase
                                                         GGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADG-VKSSIG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243
                                                                                                                                                   123 YDRYTEDREQIGRDLAQRHGLTLIPPYDHPDVLAGQGTAAKELFEEVGPLDAFFAPLGGG 182
                                                                                                                                                                                           GMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSS-IGL 246
                                                                                                                                                                                                                                                                     NTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEVK 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV 126
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                                                                                                               CEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29
6 TYDDVIAAAARIAGHANRTPVMSSRTLDEELGAEVFFKCENLQRMGAFKFRGAFNALSRF
                                     68 VPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVY
                                                                                                                                                                                                                 7 ISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRS
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                                                                                                                                                                                                                                                                                                                                               NICIVLSGGNVDL 319
                                                                                                                                                                                                                                                                                                                                                                       KNICIVLSGGNVD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RRVGVILSGGNVD 313
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- Thermotoga maritima (stra
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                       C;Species: Thermotoga maritima
C;Date: ll.Jun-1999 #sequence_revision ll.Jun-1999 #text_change 21-Jun-2002
C;Accession: D72386
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                        Nature 399, 323-329, 1999
A;Tille: Evidence for lateral gene transfer between Archaea and Bacteria from genome
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: D72386
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C; Species: Staphylococcus aureus
C; Species: 10-May-2001 #text_change 02-Aug-2002
C; Accession: F89921
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; ma, M.; Mistori-U., Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Reference number: A89758; MUID:21311952; PMID:11418146
A; Scossion: F89921
A; Stapylococcus aureus.
A; Stapylococcus aureus.
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C.Superfamily: threonine dehydratase
C.Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase;
F.51/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:BA000018; PID:g13701236; PIDN:BAB42531.1; GSPDB:GN00149 A;Experimental source: strain N315 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        185 GGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 YCEPS--DESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      244 IGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSP 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 PGDLTFELVKKYVDEMVAVNEEEIADAILFLLEQAKVVAEGAGAVGVAAVLNK----LDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13;
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37.7%; Pred. No. 1.2e-33;
Live 73; Mismatches 111;
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C;Superfamily: threonine dehydratase
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A:Status: preliminary
A:Molecule type: DNA
A:Rolecule type: Covie; A:Rolecule type: DIDI: megaplasmid pSymA
B:Galibert, F.; Finan, T.M.; Long, S.R.; Publer, A.; Abola, P.; Ampe, F.; Barloy-Hubl
Dela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.
L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A:Rolecule type: Rahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelau
A:Puble type: Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, A:Pitle: The composite genome of the legume symbiont Sinorhizobium meliloti.
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probable serine/threonine dehydratase, degradative (PA2683) [imported] - Agrobacteriu
                                         297
                                                                               71 ALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEEIANGIIATSSGNHAQGLSYAAKMLGVKVILVLPVTTPKIKIENTKALGAEVILFDG 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 AGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKIMPNLYPPETIADGVKSSI-GLNTW 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGIATAIKETKPSVRVIGAEPALTPKYFHSRV-NKERTSLPLKNTIADGLRISVPGQNPY 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 DVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIREARERLKPHVRHTPLLRAEKIEKAAGCQLYLKPETLQITGAFKIRGALNKALSL--- 65
                                         240 VK-SSIGLNTWPIIRD-LVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQH
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                                                                                                                                                                                                                 :| ||||||
----PAHIKRPLVILCGGNVD 311
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A,Genome: plasmid
C,Superfamily: threonine dehydratase
                                                                                                                                                                        298 FQTVSPEVKNICIVLSGGNVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVLSGGNWDL 312
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:56/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           threonine ammonia-lyase (EC 4.3.1.19) T01H8.2 [similarity] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C:Species: Caenorhabditis elegans C:Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 21-Jun-2002 C;Accession: T24337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 SIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVP 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 I-GLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVS 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : | |: ::: |||: |:||:||: | |: ||: | |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || | |: || |: || |: || |: || |: || |: || |: || |: || |: || |: || |: |
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A:Molecule type: DNA
A:Residues: 1-317 <WIL>
A:Residues: 1-317 <WIL>
A:Experimental source: EMBL:Z80219; PIDN:CAB02298.1; GSPDB:GN00019; CESP:T01H8.2
A:Experimental source: clone T01H8
A:Genetics:
A:Genetics:
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                                                                                                                                                                                                                                      5 YCISFADVEKAHINIRDSIHLTPVLTSSILNQ-LTGRNLFFKCELFQKTGSFKIRGALNA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
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                                                                    Length 346;
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                                                                                                                                     Indels
                                                                 Score 517; DB 2; L
Pred. No. 1.6e-32;
5; Mismatches 129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.7%; Score 514.5; DB 2; Best Local Similarity 38.0%; Pred. No. 2.2e-32; Matches 122; Conservative 61; Mismatches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted to the EMBL Data Library, September 1996 A; Reference number: 219877 A; Accession: T24337
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A;Introns: 75/3; 131/2; 159/3; 203/1; 259/3; 276/3
C;Superfamily: threonine dehydratase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase; c
C; Keywords: ammonia-lyase; carbon-nitrogen lyase
                                                                                                                           65;
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                                                             29.8%;
ilarity 37.1%;
Conservative 65
                                                             Query Match
Best Local Similarity
Matches 118; Conserv
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C; Accession: H84359
R; Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.;
A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   243 NITFPIMAGLCGKGIAVSEERALRAMVLAFNRLKVVIEPGGAVALAAAL---FHGKELES 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-495 <STO>
A; Cross-references: GB:AE004437; NID:g10581515; PIDN:AAG20244.1; GSPDB:GN00138 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADG-VKSSIG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 LNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEV 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV 126
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                                                                                                                                                                                                                                                                            C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
                                                                                                                                                  132 DESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQ-----VPLVDALVVPVGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          183 GGLTSGISLALDAKARNYKVRTAEPERFDDVARSLAAGKIERNATTSGSICDAIVTPQPG
                                                                                                        12 VEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDA
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                                                Gaps
                                         13;
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                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRC-1
      ed. No. 5.6e-31;
Mismatches 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.0%; Score 486.5; DB 2; 36.7%; Pred. No. 6e-30; Live 59; Mismatches 130;

    Halobacterium sp.

          Pred. No.
                                         48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       threonine dehydratase [imported] .
C;Species: Halobacterium sp. NRC-1
      38.78;
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300 ETVIAVASGGNVD 312
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                                      121; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 36.7
Matches 116; Conservative
      Best Local Similarity
Matches 121; Conserv
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                                                    C. Accession: A97887
R. Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Woollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A.; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum A; Reference number: A97359; PMID:11743194
A; Reference number: A9759; PMID:11743194
A; Reference number: A97689; PMID:11743194
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
Cross-references: GB:AE007869; PIDN:AAK88450.1; PID:g15157951; GSPDB:GN00169
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A; Athhors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-324 <KUR>
A.Cross-references: GB:AE008688; PIDN:AAL43716.1; PID:g17741247; GSPDB:GN00186
A.Experimental source: strain C58 (Dupont)
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 LERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | |: ||||| |: ||:| ||| |::| || |::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| || ::| ::| || ::| ::| || ::| ::| ::| || ::| ::| ::| || ::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 NITFPIMAGLCGKGIAVSEEEALRAMVLAFNRLKVVIEPGGAVALAAAL---FHGKELES 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQ-----VPLVDALVVPVGG 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADG-VKSSIG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEV 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens A;Reference number: AB2577; PMID:11743193 A;Accession: AF2912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71
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C;Species: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
Species: Agrobacterium tumefaciens
Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 VEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 28.6%; Score 496.5; DB 2; Best Local Similarity 38.7%; Pred. No. 5.6e-31; Matches 121; Conservative 48; Mismatches 131;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 KNICIVLSGGNVD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Accession: AF2912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: AGR_C_4956
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threonine ammonia-lyase (EC 4.3.1.19) [similarity] - Salmonella enterica subsp. enter C; Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi (;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 02-Aug-2002 C;Accession: AB0897 B;Parkhill, J; Dougan, G;James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A;Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                             SI-GLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AL513382; PIDN:CAD07768.1; PID:916504317; GSPDB:GN00176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L--HGDNFNDTIAK-VSEIVETEGRIFIPPYDDPKVIAGQGTIGLEIMEDLYDVDNVIVP 182
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                                                                                                                                                                                                                                                                                  62
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                                                                                                                                                                                                                                                                                  3 VSLADIQAAAVRLKGSAVETPLIESPALNDRLGGRIFLKPETLQRAGAFKFRGAYNRLSQ
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                                                                                                                          .2e-29;
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                                                                                                                                                        Mismatches
                                                                                          Score 479.5;
Pred. No. 1.2
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C;Superfamily: threonine dehydratase
                                threonine dehydratase
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                                                                                          27.6%;
llarity 34.7%;
Conservative 6
                                                                                                                    Best Local Similarity
Matches 110; Conserv
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A; Residues: 1-329 <PAR>
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   A;Gene: CC3105
C;Superfamily:
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                                                                                             Query Match
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                                                                                                                                                                                                                                  Cispecies: Sulfolobus solfataricus
Cispecies: Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A: Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: D90166
A; Status: preliminary
A; Accession: D90166
A; Residues: 1-405 < CURA
A; Residues: 1-405 < CURA
A; Cross-references: GB: AEO06641: NID: g13813385; PIDN: AAK40587.1; GSPDB: GN00155
C; Genetics:
A; Geneti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              threonine dehydratase [imported] - Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Species: Caulobacter crescentus
C; Sate: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 31-Dec-2001
C; Accession: G87633
R; Nierman, W.C; Feldblyum, T.V; Paulsen, I.T; Nelson, K.E; Eisen, J.; Heidelberg, J. B.; Laub, M.T; DeBoy, R.T; Dodson, R.J; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. A.Title: Complete Genome Sequence of Caulobacter crescentus.
A; Reference number: A87249; MUID:21173698; PMID:11259647
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A; Residues: 1-325 <STO>
A; Cross-references: GB:AE005673; NID:g13424763; PIDN:AAK25067.1; GSPDB:GN00148
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             184 VGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADG--VK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     242 SSIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTV 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 YCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAV 64
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                                                                                                                                                                                                                  hypothetical protein tdcB [imported] - Sulfolobus solfataricus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   288 SGKVKVNGIDKKVISLVSGGNIDLSLLSTLT 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            302 SPEV-----KNICIVLSGGNVDLT--SSIT 324
                                | | | | ||:||
381 E--TIVPALCGGNIDL 394
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09hlw2 thermoplasm 08hlw2 thermoplasm 08rdt9 fusobacteri 082x16 pyrobaculum 082x18 salmonella 092hz2 rickettsia 09160 pseudomonas 08x9v3 yersinia pe 09hhf0 drosophila 09pp95 campylobact 08u6p8 agrobacteri 09pp95 campylobact 08u6p8 agrobacteri 09rwu8 deinococcus 09xv8 caenorhabdi 095x9 caenorhabdi 095x9 caenorhabdi 095x9 caenorhabdi 095x9 caenorhabdi

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Q9t0dl arabidopsis	Q8xpx0 ralstonia s	Q8x0j0 neurospora	Q9i0f5 pseudomonas	09xaa4 streptomyce	Q9wyjl thermotoga	099u50 staphylococ	093968 caenorhabdi	Q92y58 rhizobium m	Q8x177 clostridium	Q975y3 sulfolobus	. Q8ubw5 agrobacteri	Q9ewq3 streptomyce	Q9hnh6 halobacteri	0980pl sulfolobus	097cb2 thermoplasm
QI	Q9T0D1	Q8XPX0	Q8X0J0	Q910F5	Q9XAA4	Q9WYJ1	099050	896860	Q92Y58	08XL77	0975x3	Q8UBW5	Q9EWG3	9HNH6O	Q980P1	Q97CB2
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% Nuery Aatch Length DB	346	323	388	320	325	401	346	317	323	402	404	324	409	495	405	406
% Query Match	46.3	34.7	31.7	31.1	30.8	30.7	29.8	29.7	29.3	28.8	28.7	28.6	28.0	28.0	27.8	27.7
Score	802.5	602	550	539	535	532.5	517	514.5	508.5	499	497.5	496.5	486.5	486.5	483	480.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELFQKTGSFKIRGALNAVRSL-VPDALE-RKPKAVVTHSSGNHGQALTYAAKLEGIPAYI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVPQTAPDCKKLAIQAYGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGGG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAALELQRQVAASLSTSGTTTTTNRRRLNAIITPCGGGGLLSGTALACSDLSPSDPSTPG 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -VKVYAAEP--SNADDCYQSKLKGKLMPNLYPPETIADGVKSSIGLNTWPII--RDLVDD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PILVFGAEPSFSGADDGRRGYYSGTRIESV-KSLTIADGLRTPLGAYPWSIIYERKLVAG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----NLFFKC 46
                                                                YCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGG
                                                                                                      GGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSS-IG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 388;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Nyakatura G., Mewes H.W., Mannhaupt G.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Best Local Similarity 37.9%; Pred. No. 6.9e-36;
Matches 140; Conservative 62; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 ADVEKAHINIRDSIHLTPVLTSSILNQLTGR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                German Neurospora genome project;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
BMBL; AL670005; CAD21283.1; --
InterPro; IPR001926; B6_enzyme_beta.
                                                                                                                                                                                                                                                                                                                         388 AA
                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLEE). 20, Last
01-JUN-2002 (TrEMBLEE). 21, Last
Nealted to threonine dehydratase.
B11H24.140.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41505 MW;
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299 KRVGVIISGGNVDL 312
                                                                                                                                                                                                                      KNICIVLSGGNVDL 319
                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schulte U., Aign V.,
Nyakatura G., Mewes H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00291; PALP;
SEQUENCE 388 AA; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                   Q8X0J0;
01-MAR-2002
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                                            127
                                                                         123
                                                                                                     187
                                                                                                                                   183
                                                                                                                                                                                        242
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                                                                                                                                                                                                                                                                                                                                               TLPVINTIADGLRASLGDLTWPVVRDLVDDVVTLEECEIIEAMKMCYEILKVSVEPSGAI 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                         --KTGSFKIRGALNAVRSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQ :108
                                                                                                                                                                         67 CGKSGAFKFRGACNAVLSL--DA-EQAAKGVVTHSSGNHAAALSLAAKIQGIPAYIVVPK 123
                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIV 126
                                                                                                                              99
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                                                                                                                                                                                                                                  TAPDCKKLAIQAYGASIVYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIAL
                                                                                                                                                                                                                                                                         EVLNQVPLVDALVVPVGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMP
                                                                                                                                                                                                                                                                                                                                NLYPPETIADGVKSSIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chondler M., Choisne N., Claudel Renard C., Cunnac S., Demange N. Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002)
                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
8
                                           DB 10; Length 346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group;
                                                                                                QYCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
              47C37E1CA52B91F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2175CBF693E04A2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; beta subdivision; Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Probable amino-acid dehydratase protein (EC 4.2...).
RSP1516 OR RS04793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                                                                                                                                                                                                                                                       GVAAVLSQHFQTVSP---EVKNICIVLSGGNVDLTS 321
                                                                                                                                                                                                                                                                                                                                                                                                         Score 802.5; DB 10;
Pred. No. 3.3e-56;
67; Mismatches 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 602; DB 16;
Pred. No. 3.6e-40;
5; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macute 110.00 CAD18667.1; -- EMBL, AL646685, CAD18667.1; -- Pfan, PF001926; B6_enzyme_beta. Pfan, PF00291; PALP; 1. Lyase; Plasmid, Complete proteome. SEQUENCE 323 AA; 34515 MW; 2175C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21681879; PubMed-11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65;
 l protein.
346 AA; 36839 MW;
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                                         46.3%;
                                                                    Matches 163; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                     Similarity
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Hypothetical
SEQUENCE 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ralstonia
                                                                                                                                                                                                                                                                                                                                                                                       289
                                         Query Match
Best Local (
                                                                                                                                                                                                                109
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124; Conservative
                                                         Streptomyces coelicolor.
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                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                          STRAIN=A3(2);
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVY 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSS-IGL 246
312 MYSVGEEEIKKALRLVYERMKVVVEPSAVVGLAVALFNEEFRSMVEREGGEEGWDLGVVF 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

MEDLINE-2043737; Pubmed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnaqle W.O., Kowalik D.J., Lagrou M., Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim, R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E. W., Lory S., Olson M.V.; "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8 SFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8;
                                                                                                                                                                                         Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 31.1%; Score 539; DB 16; Length 320; Best Local Similarity 38.0%; Pred. No. 4e-35; Matches 119; Conservative 66; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              320 AA; 33957 MW; C6F97C6259FE8584 CRC64;
                                                                                                                       01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Probable serine/threonine dehydratase, degradative.
                                                                                                   320
                                                                                                                                                                                                                                                                                                                                                                   MBCLE AROUGE96; AAG06071.1; -. HSSP; P04968; 1TDJ. InterPro; IPR001926; B6_enzyme_beta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           307 NICIVLSGGNVDL 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                opportunistic pathogen."
                                                                                                                                                                                                                                                                                                                                                             Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00291; PALP; 1.
Complete proteome.
                                   SGGNVDLTS 321
                                                                                                                                                                                Pseudomonas aeruginosa
                                                                                                                                                                                                          NCBI_TaxID=287;
                                                                                                                                                                                                      Pseudomonas
                      313
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GGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADG-VKSSIG: 245
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STRAIN-A3(2) / M145;

Bentley S.D., Chateck K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Bentley S.D., Chateck K.B., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Nell S.,
Rabbinowitsch E., Rajaddram M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
Warten T., Wletzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.; As et of ordered cosmids and a detailed genetic and physical map ithe 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces.
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'Complete genome sequence of the model actinomycete Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=A3(2);
James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                              Seeger K., Harris D.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coelicolor A3(2).";

Nature 417:141-147(2002).

EMBL; AL09683: CAB48898.1; -

HSSP; P04968: 1TDJ.

InterPro; IPR001926; B6_enzyme_beta.

InterPro; IPR000634: S/T_dehydrtse.

Pfam; PF00291; PALP; DEPTDRATASE_SER_THR; 1.

PROSITE; PS000165; DEPTDRATASE_SER_THR; 1.

SEQUENCE 325 AA; 33965 MW; 4EIDE62D340489A7 CRC64;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.8%; Score 535; DB 16; 39.6%; Pred. No. 8.5e-35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=A3(2);
MEDLINE=97000351; PubMed=8843436;
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                                                                                                  Putative threonine dehydratase sco0821 or scF43A.11C.
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Query Match
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Q99U50;
                                      RESULT 7
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244 ELTFSLNRRLLDGIVLVSDDEIRDAMRFAFERLKTVLEPSGATPLAALLNGRIDALP--- 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 IGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSP 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 YCEPS--DESRENVAKRVTEETEGIMVHPNQEPAVIAGOGTIALEVLNQVPLVDALVVPV 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 GGGGLISGVSVAIKSMNPEVKVIGVQTENMPSMIASLRRGR-AERVEGKPTLADGIAVKK 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7 ISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
"Evidence for lateral gene transfer between Archaea and Bacteria from
genome sequence of Thermotoga maritima.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermotoga maritima.
Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
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                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73; Mismatches 111;
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                                                                                                                                                                                                                                                                                401 AA
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PROSITE: PSO0165; DEHYDRATASE_SER_THR; 1.
Complete proteome. 43110 WW, 4D757A8F83:
SEQUENCE 401 AA; 43110 WW, 4D757A8F83:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002912; ACT.
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
Pfam; PF01842; ACT; 1.
Pfam; PF00291; PALP; 1.
                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-MSB8 / DSM 3109;
MEDLINE-99287316; PubMed-10360571;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Threonine dehydratase catabolic
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KGKKVAIVISGGNIDV 307
                                                                                            301 RRVGVILSGGNVD 313
                                                            KNICIVLSGGNVD 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 119; Conservative
                                                                                                                                                                                                                                                                                PRELIMINARY;
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189 VGGGGLIAGIATALKSFNPSIHIIGVQAENVHGMAESFYKRALTEH-REDSTIADGCDVK 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPECIES-S.aureus (strain MuSO), and S.aureus (strain N315);
MEDLINE-21311952; PubMed=114.88146;
Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Mizutahi-Ui Y., Takahashi N.K., Sawno T., Inoue R.T., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba 'Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
"Whole genome sequencing of meticillin-resistant Staphylococcus aureus."
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9
                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus aureus (strain Mu50 / ATCC 700699), and
Staphylococcus aureus (strain N315).
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 346;
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                                                                                                                                                    01.JUN-2001 (TrEMBLrel. 17, Last sequence update) 01.JUN-2002 (TrEMBLrel. 21, Last annotation update) 8A1271 protein (Threonine deaminase IlvA homolog). SAV1438 OR SA1271.
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346 AA.
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PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
                                                                                                            Created)
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InterPro; IPR000634; S/T_dehydrtse.
PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AP003362; BAB57600.1; -. EMBL; AP003133; BAB42531.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus.
NCBI_TaxID=158878, 158879;
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Matches 118; Conservative
PRELIMINARY;
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Q93968;
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AC 09
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                   VK-SSIGLNTWPIIRD-LVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQH 297
                                                                                                                                                                                                                                                                                                                                                                RSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGAS 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ISFADVEKAHINIRDSIHLTPVLTSSILNQLTGR--NLFFKCELFQKTGSFKIRGALNAV
                                                                                                                                                                                                                                                                                                                                     VGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPP----ETIADG
                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                  Length 317;
                                                                                                                                                                      Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                      Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                              OFODE6C7479389E3 CRC64;
          Last sequence update)
Last annotation update)
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Last annotation update)
                                                                                                                                                                                                                                                                                  DB 5;
                                                                                                                                                                                                                                                                                                     61; Mismatches 115;
                                                                                                                                                                                                                                                                                 29.7%; Score 514.5; DB 538.0%; Pred. No. 3.6e-33;
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01-DEC-2001 (TrEMBLrel. 19, Last sequence upo
01-MAR-2002 (TrEMBLrel. 20, Last annotation on the putative threonine dehydratase.
RA1030 OR SWA1872.
Rhizobium meliloti (Sinorhizobium meliloti).
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                                                                                                                                                                                                                   InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
Pfam; PF00291; PALP; 1.
PRO$T10015; DEHYDRATASE_SER_THR; 1.
SEQUENCE 317 AA; 34688 MW; 0F0DE6C747
   Created)
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----PAHIKRPLVILCGGNVD 311
                                                                                                                                                   MEDLINE-99069613; PubMed-9851916;
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                                                                                                                                                                                investigating biology.";
Science 282:2012-2018(1998).
EMBL: 280219; CAB02298.1; --
HSSP; P35520; 1JBQ.
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NCBI_TaxID=382;
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01-FEB-1997 (TrEMBLrel. 01-FEB-1997 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                 Caenorhabditis elegans.
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Matches 122; Conserv
                                                                                                                                         SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                                                 SEQUENCE FROM N.A.
                                                                              NCBI_TaxID=6239;
                              T01H8.2 protein.
                                                                                                              Cennard N.;
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71 ALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEP 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVKSSI-GLNTW 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGIATAIKETKPSVRVIGAEPALTPKYFHSRV-NKERTSLPLKNTIADGLRISVPGQNPY 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 DVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barnett M.J., Fisher R.F., Jones T., Komp C., Abola A.P.,
Barloy-Hubler F., Bowser L., Capela D., Galibert F., Gouzy J.,
Gurjal M., Hong A., Huizar L., Hyman R.W., Kahn D., Kahn M.L.,
Kalman S., Keating D.H., Palm C., Peck M.C., Surzycki R., Wells D.H.,
Yeh K.-C., Davis R.W., Federspiel N.A., Long S.R.;
"Nucleotide sequence and predicted functions of the entire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 323;
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Clostridium perfringens.
Bacteria; FirmLoutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.3%; Score 508.5; DB 16; Length 36.8%; Pred. No. 1.1e-32; ive 62; Mismatches 127; Indels
                                                                                                                                                                                                                    Sinorhizobium mellioti psyma megaplasmid.";
Proc. Natl. Acad. Sci. U.S.A. 98:9883-9888(2001).
BMBL; AE007289; AAK656881;
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR001926; B6_enzyme_beta.
PROSITE; PS00165; DEHYDRATASE_SER_THR; UNKNOWN_I.
PROSITE; PS00165; DEHYDRATASE_SER_THR; UNKNOWN_I.
Plasmid; Hypothetical protein; Complete proteome.
SEQUENCE 323 AA; 34706 MW; 1BF363B67F4D635B CRC64;
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Last annotation update)
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Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP003189; BAB80871.1;
InterPro: IPR002912; AcT.
InterPro: IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
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MEDLINE=21396509; PubMed=11481432;
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Matches 114; Conservative
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PubMed=11792842;
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Q8UBW5;
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6
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                                                                                                                                                                                             SRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVGGGGMLAGI 193
                                                                                                                                                                                                                                                         187
                                                                                                                                                                                                                                                                                                                                          14 KAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDALE 73
                                                                                                                                                          67
                                                                                                                                              194 AITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADGVK-SSIGLNTWPII
                                                                                                                                                                                                                                                                                             : '||| |:||| : |: :| |::: | :|||||: | TLAAKALNPNVKVIGVQAEGANAMVKSFKAGEIIA-LDAVDTIADGIAVKRPGDLTFKFI
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EMBL. ADOO0982; Baba5265.1; --

EMBL. ADOO0982; Baba5265.1; --

EMBL. PRO01926: B6_enzyme_beta.
                                                                                                            Gaps
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                                                                                   Length 402;
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                                                                                                        68; Mismatches 124; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGREAMS; TIGRO1127; inva_lcterm; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 404 AA; 44034 MW; 4C4B44D776FE26B7 CRC64;
                                                          402 AA; 43421 MW; E872AC5FE71BF809 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                28.8%; Score 499; DB 16; 36.3%; Pred. No. 8.9e-32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               404 AA.
          Pfam; PF00291; PALP; 1.
TIGRFAMs; TIGR01127; ilva_lCterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
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                                                                                                                                                                                                                                                                                                                                                                             SGGNVDLTSSITWVKQA 329
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                                                                                             Best Local Similarity 36.39
Matches 115; Conservative
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Pfam; PF01842; ACT; 1.
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PubMed=11572479;
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                                              Complete proteome.
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Matches 130; Conserv
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IV-YCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVP 183
                                                                                                                                                                                                                                                                                                                                                           VGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADG--VK 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSIGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTV 301
                                  3 YTKYFDEIVKIQDRIKQYIHETPIDYSKTFSDMIGAQIYLKLENLOKTGSFKVRGAFSKL 62
                                                                                                                     RSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-21608551; PubMed=11743194;
MEDLINE-21608551; PubMed=11743194;
Goodner B., Hinkle G., Gattung S., Miller N., Halling C., Mullin L., Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F., Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B., Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G., Cielo C., Slater S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr., Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C., Kutyavin T., Levy R., Li M.-J., McClelland E., Palmieri A., Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D. Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Nester E.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILVA OR ATUZ735 OR AGR_C_4956.
Agrobacterium tumefaciens (strain C58 / ATCC 33970).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogen and biotechnology agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the plant |
Agrobacterium tumefaciens C58.
Science 294:2323-2328(2001).
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us-09-889-609b-10.rspt

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InterPro; IPR002912; ACT.
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
Pfam: PF01842; ACT; 1.
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                                  EMBL; AL51182; CAC18697.1; -. EMBL; AL512667; CAD30948.1; -.
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      Nature 417:141-147(2002)
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ILUA OR VNG2100G.
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                                                                                                   HSSP; P04968;
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                                                                                                                                                                                                                                                                                                                               186
                                                                                                                                                                                                                                                                                                                                                                                   124 NEDRDAIGNRESSERGLTLIRPYDEPLVIAGQGTAGLEIAEQGAELGIGAAEVL-VPCGG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADG-VKSSIG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 LNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSPEV 305
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                                                                    71
                                                             VEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRSLVPDA
                                                                                                                                                                                                LERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGASIVYCEPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 NITFPIMAGLCGKGIAVSEEFALRAMVLAFNRLKVVIEPGGAVALAAAL---FHGKELES
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"A set of ordered cosmids and a detailed genetic and physical map for the B Mb Streptomyces coelicolor 73(2) chromosome.";
Mol. Microbiol. 21:77-96(1996).
                                                                                                                           7 IEAARERIGNHAVRTPLLTSPFLDEIAGRKLFVKAECLQRTGSFKFRGGWSAVSGLPADV
   13; Gaps
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Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
Rabbinowitsch E., Rajandram M.A., Rutherford K., Rutter S.,
Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,
Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of the model actinomycete Streptomyces coelicolor {\rm A3(2)."},
   Mismatches 131; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oliver K., Harris D.;
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative amino acid deaminase.
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MEDLINE=97000351; Pubmed=8843436;
48;
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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Matches
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MEDLINE=20504483: PubMed=11016950;
My W.V. Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
Genome sequence of Halobacterium species NRC-1.";
Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 VYCEPSDESRENVAKRVTEETEGIMVHPNQEPAVIAGQGTIALEVLNQVPLVDALVVPVG
                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                                                                       Length 409;
                                                                                                                                                                                                                                                                                                                                       129; Indels
                                                                                              TIGRFAMS; TIGR01127; iiva_lcterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; 1.
Hypothetical protein; Complece protecome.
SEQUENCE 409 AA; 42279 MW; 9F21A40D3ECEA9B9 CRC64;
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Halobacteriaceae; Halobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                       DB 16;
                                                                                                                                                                                                                                                                Query Match 28.0%; Score 486.5; DB 1
Best Local Similarity 38.2%; Pred. No. 9.1e-31;
Matches 120; Conservative 54; Mismatches 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       495
InterPro; IPR001926; B6_enzyme_beta.
InterPro; IPR000634; S/T_dehydrtse.
Pfam; PF00291; PALP; 1.
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STRAIN-ATC 35092 / DSM 1617 / P2;
STRAIN-ATC 35092 / DSM 1617 / P2;
MEDLINE-21332296; PubMed-11427726;
She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
Thi Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
Charlebois R.L., Doolitle W.F., Duguet M., Gaasterland T.,
Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
"The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
"The Complete Sci. U.S.A. 98:7835-7840(2001).
                                                                                                                                                               7 ISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAVRS
                                                                                                                                                                                                                                                                                                                                                             GGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYP-PETIADGVK-SS
                                                                                                                                                                                                                                                                                                                                                                                 IGLNTWPIIRDLVDDIFTVTEDEIKCATQLVWERMKLLIEPTAGVGVAAVLSQHFQTVSP
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sulfolobus solfataricus.
Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2011 (TrEMBLrel. 18, Last sequence update)
01-UJNN-2020 (TrEMBLrel. 18, Last annotation update)
Threonine dehydratase catabolic (threonine deaminase) (tdcB) (EC
                                                                                                                                  11;
                                                                                                 DB 17; Length 495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 483; DB 17; Length 405; Pred. No. 1.7e-30;
                                                                                                                                  Indels
               TIGRFAMS; TIGRO1127; ilva_lCterm; 1.
PROSITE; PS00165; DEHYDRATASE_SER_THR; UNKNOWN_1.
Complete Proteome.
SEQUENCE 495 AA; 53095 WW; 8F203680AAF93F80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lyase; Complete proteome.
SEQUENCE 405 AA; 44363 MW; F1266A940110B062 CRC64;
                                                                                               Query Match 28.0%; Score 486.5; DB 17; Best Local Similarity 36.7%; Pred. No. 1.2e-30; Matches 116; Conservative 59; Mismatches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      405 AA.
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InterPro; IPR002912; ACT.
InterPro; IPR001926; B6_enzyme_beta.
Pfam: PF001842; ACT: 1.
Pfam: PF00291; PALP; 1.
TIGRFAMS; TIGR01127; ilva_lCterm; 1.
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Pfam; PF00291; PALP; 1.
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Best Local Similarity
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                                                                                                           65 RSLVPDALERKPKAVVTHSSGNHGQALTYAAKLEGIPAYIVVPQTAPDCKKLAIQAYGAS 124
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                                                       3 YLEYFDRIRLAKEKIEKYVHITPIDYSTTFSRIINAKVYLKLENLQKTGSFKVRGAFNKL
                                     5 YCISFADVEKAHINIRDSIHLTPVLTSSILNQLTGRNLFFKCELFQKTGSFKIRGALNAV
                                                                                                                                                                                                                                                    184 VGGGGMLAGIAITVKALKPSVKVYAAEPSNADDCYQSKLKGKLMPNLYPPETIADG--VK
   Gaps
 26;
 Mismatches 115; Indels
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